

STN Columbus

* * * * * Welcome to STN International * * * * *

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America
 NEWS 2 "Ask CAS" for self-help around the clock
 NEWS 3 FEB 25 CA/CAPLUS - Russian Agency for Patents and Trademarks
 (ROSPATENT) added to list of core patent offices covered
 NEWS 4 FEB 28 PATDPAFULL - New display fields provide for legal status
 data from INPADOC
 NEWS 5 FEB 28 BABS - Current-awareness alerts (SDIs) available
 NEWS 6 FEB 28 MEDLINE/LMEDLINE reloaded
 NEWS 7 MAR 02 GBFULL: New full-text patent database on STN
 NEWS 8 MAR 03 REGISTRY/ZREGISTRY - Sequence annotations enhanced
 NEWS 9 MAR 03 MEDLINE file segment of TOXCENTER reloaded
 NEWS 10 MAR 22 KOREAPAT now updated monthly; patent information enhanced
 NEWS 11 MAR 22 Original IDE display format returns to REGISTRY/ZREGISTRY
 NEWS 12 MAR 22 PATDPASPC - New patent database available
 NEWS 13 MAR 22 REGISTRY/ZREGISTRY enhanced with experimental property tags
 NEWS 14 APR 04 EPFULL enhanced with additional patent information and new
 fields
 NEWS 15 APR 04 EMBASE - Database reloaded and enhanced
 NEWS 16 APR 18 New CAS Information Use Policies available online
 NEWS 17 APR 25 Patent searching, including current-awareness alerts (SDIs),
 based on application date in CA/CAPLUS and USPATFULL/USPAT2
 may be affected by a change in filing date for U.S.
 applications.
 NEWS 18 APR 28 Improved searching of U.S. Patent Classifications for
 U.S. patent records in CA/CAPLUS
 NEWS EXPRESS JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT
 MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
 AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005
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 NEWS PHONE Direct Dial and Telecommunication Network Access to STN
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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 15:37:06 ON 29 APR 2005

=> file registry		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'REGISTRY' ENTERED AT 15:37:19 ON 29 APR 2005
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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

Please note that search-term pricing does apply when conducting SmartSELECT searches.

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*****
*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*
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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

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=> s ctggctgc/sqsn and SQL<=375
SYSTEM LIMITS EXCEEDED - SEARCH ENDED
The search profile you entered was too complex or gave too many
answers. Simplify or subdivide the query and try again. If you have
exceeded the answer limit, enter DELETE HISTORY at an arrow prompt
(=>) to remove all previous answers sets and begin at L1. Use the
SAVE command to store any important profiles or answer sets before
using DELETE HISTORY.
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=> s ctggctgc/sqen
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=> s 14 and SQL<=375
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STN Columbus

21132138 SQL<=375
L5 190 L4 AND SQL<=375

=> file caplus; s 15 and PY<1990
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FILE 'CAPLUS' ENTERED AT 15:41:43 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

106 L5
13008711 PY<1990
L6 0 L5 AND PY<1990

=> s 14
L7 1010 L4

=> s 17 and PY<1990
13008711 PY<1990
L8 3 L7 AND PY<1990

=> d bib ab hitstr

L8 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS
DN 120:296653
TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum
IN Houghton, Michael; Choo, Qui Lim; Kuo, George
PA Chiron Corp., India
SO Indian, 157 pp.
CODEN: INXXAP
DT Patent
LA English
FAN.CNT 8

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PL, RO, SD, SU				
RW: BF, BJ, CF, CG, CM, GA, ML, MR, SN, TD, TG				
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STN Columbus

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US 6074816	A	20000613	US 1994-307273	19940916
US 5712087	A	19980127	US 1995-440519	19950512
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JP 09173079	A2	19970708	JP 1996-241451	19960822
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GR 3031361	T3	20000131	GR 1999-402455	19990929
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JP 1993-178446	A3	19881118		
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JP 1998-111631	A3	19881118		
WO 1988-US4125	A	19881118		
YU 1986-2138	A6	19881118		
US 1989-325338	B2	19890317		
US 1989-341334	B2	19890420		
US 1989-353896	B2	19890421		
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NO 1989-2931	A	19890717		
US 1989-398667	B2	19890825		
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US 1990-504352	A	19900404		
US 1990-505435	B2	19900404		
US 1990-566209	B1	19900808		
US 1990-611965	B2	19901108		
WO 1991-US2225	A	19910329		
EP 1991-302910	A3	19910403		
US 1992-910760	A3	19920707		
US 1993-40564	A3	19930331		
US 1993-103961	A1	19930809		
US 1994-306472	A3	19940915		
US 1994-307273	A3	19940916		
AB	The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated			

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from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ -gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-86-8

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

STRUCTURE DIAGRAM IS NOT AVAILABLE

=> d bib ab seq 1-3

'SEQ' IS NOT A VALID FORMAT FOR FILE 'CAPLUS'

The following are valid formats:

ABS ----- GI and AB
ALL ----- BIB, AB, IND, RE
APPS ----- AI, PRAI
BIB ----- AN, plus Bibliographic Data and PI table (default)
CAN ----- List of CA abstract numbers without answer numbers
CBIB ----- AN, plus Compressed Bibliographic Data
DALL ----- ALL, delimited (end of each field identified)
DMAX ----- MAX, delimited for post-processing
FAM ----- AN, PI and PRAI in table, plus Patent Family data
FBIB ----- AN, BIB, plus Patent FAM
IND ----- Indexing data
IPC ----- International Patent Classifications
MAX ----- ALL, plus Patent FAM, RE
PATS ----- PI, SO.
SAM ----- CC, SX, TI, ST, IT
SCAN ----- CC, SX, TI, ST, IT (random display, no answer numbers;
SCAN must be entered on the same line as the DISPLAY,
e.g., D SCAN or DISPLAY SCAN)
STD ----- BIB, IPC, and NCL

IABS ----- ABS, indented with text labels
IALL ----- ALL, indented with text labels
IBIB ----- BIB, indented with text labels
IMAX ----- MAX, indented with text labels
ISTD ----- STD, indented with text labels

OBIB ----- AN, plus Bibliographic Data (original)
OIBIB ----- OBIB, indented with text labels

SBIB ----- BIB, no citations
SIBIB ----- IBIB, no citations

HIT ----- Fields containing hit terms
HITIND ----- IC, ICA, ICI, NCL, CC and index field (ST and IT)
containing hit terms
HITRN ----- HIT RN and its text modification
HITSTR ----- HIT RN, its text modification, its CA index name, and
its structure diagram
HITSEQ ----- HIT RN, its text modification, its CA index name, its
structure diagram, plus NTE and SEQ fields
FHITSTR ----- First HIT RN, its text modification, its CA index name, and

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its structure diagram
 FHITSEQ ----- First HIT RN, its text modification, its CA index name, its
 structure diagram, plus NTE and SEQ fields
 KWIC ----- Hit term plus 20 words on either side
 OCC ----- Number of occurrence of hit term and field in which it occurs

To display a particular field or fields, enter the display field
 codes. For a list of the display field codes, enter HELP DFIELDS at
 an arrow prompt (=>). Examples of formats include: TI; TI,AU; BIB,ST;
 TI,IND; TI,SO. You may specify the format fields in any order and the
 information will be displayed in the same order as the format
 specification.

All of the formats (except for SAM, SCAN, HIT, HITIND, HITRN, HITSTR,
 FHITSTR, HITSEQ, FHITSEQ, KWIC, and OCC) may be used with DISPLAY ACC
 to view a specified Accession Number.
 ENTER DISPLAY FORMAT (BIB):bib ab hitseq

L8 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS
 DN 120:296653
 TI A method for preparing a kit for the detection of antibodies to HCV
 (hepatitis C virus) in biological samples such as blood serum
 IN Houghton, Michael; Choo, Qui Lim; Kuo, George
 PA Chiron Corp., India
 SO Indian, 157 pp.
 CODEN: INXXAP
 DT Patent
 LA English
 FAN.CNT 8

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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STN Columbus

WO 9115771	A1	19911017	WO 1991-US2225	19910329
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RW: BF, BJ, CF, CG, CM, GA, ML, MR, SN, TD, TG				
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STN Columbus

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US 1994-306472	A3	19940915
US 1994-307273	A3	19940916

AB The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ -gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-86-8

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

SEQ 1 ctggctgcgt ggctcatagtg ggcagggctcg tcttgctcgg gaagccggca
51 atcatacctg acagggaagt cctctaccga gagttcgatg agatggaaga
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201 gaggttatcg cccctgctgt ccagaccaac tggcaaaaac tcgagacctt
251 ctgggcgaag catatgtgga acttcatcag tgggatacaa tacttggcgg
301 gcttgtaaac gctgcctggg aaccccgcca ttgcttcatt gatggctttt
351 acagctgctg tcaccagccc actaaccact agccaaa

L8 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

STN Columbus

AN 1989:401656 CAPLUS
 DN 111:1656
 TI The sequence of hemC, hemD and two additional E. coli genes
 AU Alefounder, Peter R.; Abell, Chris; Battersby, Alan R.
 CS Chem. Lab., Univ. Cambridge, Cambridge, BCB2 1EW, Guatemala
 SO Nucleic Acids Research (1988), 16(20), 9871
 =====
 CODEN: NARHAD; ISSN: 0305-1048
 DT Journal
 LA English
 AB A 4260-bp sequence from Escherichia coli contg. the porphobilinogen
 deaminase gene hemC, the uroporphyrinogen III cosynthetase gene hemD plus
 2 more genes X and Y is presented. Genes hemC, hemD, and X are all part
 of the Uro operon.
 IT 104708-82-9, Deoxyribonucleic acid (Escherichia coli clone pLC41-4
 gene hemC)
 RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)
 RN 104708-82-9 CAPLUS
 CN DNA (Escherichia coli clone pLC41-4 gene hemC) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggttagaca atgttttaag aattgccaca cgccaaagcc cacttgcaact
 51 ctggcaggca cactatgtca aagacaagtt gatggcgagc catccggggcc
 101 tgggtcgttga actggtaccg atggtgacgc gcggcgatgt gattcttgat
 151 acgccgctgg cgaaagtagg cggaaaaggc ttatttgtaa aagagctgga
 201 agtcgcgctc ctgaaaatc gcgccgatat cgccgtacac tcaatgaaag
 251 atgtgccggt tgaattcccc caaggctctg gactggtcac tatttgtagg
 301 cgtgaagatc ctgcgcatgc ctttgtgtcc aataactatg acagtctgga
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 801 cggttcgcag attattcgcg gtgaacgcgc cgggtgcgcg caagatgccg
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 901 gagatcctcg ctgaagtcta taacggagac gccccggcat ga

L8 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:565982 CAPLUS
 DN 105:165982
 TI Nucleotide sequence of the hemC locus encoding porphobilinogen deaminase
 of Escherichia coli K12
 AU Thomas, Steven D.; Jordan, Peter M.
 CS Dep. Biochem., Univ. Southampton, Southampton, SO9 3TU, UK
 SO Nucleic Acids Research (1986), 14(15), 6215-26
 =====

CODEN: NARHAD; ISSN: 0305-1048
 DT Journal
 LA English
 AB Porphobilinogen deaminase [9074-91-3], the product of the hemC locus in
 E. coli K12, catalyzes the tetrapolymn. of porphobilinogen (PBG) into the
 hydroxymethylbilane, preuroporphyrinogen. The hemC locus was subcloned

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from the Clarke and Carbon plasmid pLC41-4. The sequence of the hemC structural gene and flanking DNA was detd. by the dideoxy chain-termination method of Sanger. The structural gene for hemC is located within a 942-base-pair sequence encoding the monomeric PBG deaminase, mol. wt. 33,857. The extent of the coding region was confirmed by sequencing the N-terminus of the purified enzyme and by detn. of the mol. wt. The hemC locus is closely linked to the cyaA locus, the genes being transcribed in a divergent manner. Upstream of the hemC coding region, a possible promoter and 3 repeated GGATG sequences were identified. This is the 1st report of a complete DNA sequence for a structural gene specifying an enzyme of the heme biosynthetic pathway in prokaryotes.

IT 104708-82-9

RL: FRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 104708-82-9 CAPLUS

CN DNA (Escherichia coli clone pLC41-4 gene hemC) (9CI) (CA INDEX NAME)

NTE doublestranded

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     351 tgcgttaccg gcaggcagta tcgtcgggac gtccagttta cgtcgccagt
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=> s 15

L9 106 L5

=> s 15 and PY<1991

106 L5

13523241 PY<1991

L10 0 L5 AND PY<1991

=> s 15 and PY<1991

13523241 PY<1991

L11 0 L9 AND PY<1991

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151946 SQL=10
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L15 ANSWER 1 OF 64 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1996:702025 CAPLUS

DN 125:58866

TI DNA encoding various truncated and mutein forms of human and murine colony stimulating factor-1

IN Ladner, Martha B.; Noble, Janelle A.; Martin, George A.; Kawasaki, Ernest S.; Coyne, Mazie Y.; Halenbeck, Robert F.; Koths, Kirston E.

PA Celus Oncology Corp., USA

SO U.S., 45 pp., Cont.-in-part of U.S. Ser. No. 799, 039, abandoned.

CODEN: USXXAM

DT Patent

LA English

PAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5573930	A	19961112	US 1992-999298	19921228
	CA 1339873	A1	19980519	CA 1986-500902	19860131
	ES 551665	A1	19870301	ES 1986-551665	19860205 <--
	ZA 8690839	A	19871028	ZA 1986-839	19860205 <--
	ZA 8707979	A	19890628	ZA 1987-7979	19871023 <--
	AT 105869	E	19940615	AT 1987-309409	19871023
	IL 84257	A1	19970218	IL 1987-84257	19871023
	US 4847201	A	19890711	US 1988-157094	19880209 <--
	US 5470569	A	19951128	US 1994-212300	19940314
	US 5556620	A	19960917	US 1994-220454	19940331
	US 5614183	A	19970325	US 1995-371803	19950111
	US 5635175	A	19970603	US 1995-371804	19950111
	US 5837229	A	19981117	US 1995-371805	19950111
	US 5681719	A	19971028	US 1995-401013	19950308
	US 6204020	B1	20010320	US 1995-401632	19950309
	US 5642563	A	19970701	US 1995-426036	19950421
	US 5672343	A	19970930	US 1995-426279	19950421
	US 6103224	A	20000815	US 1995-426570	19950421
	US 6117422	A	20000912	US 1995-425876	19950421
	US 6146851	A	20001114	US 1995-426243	19950421

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	US 6156300	A	20001205	US 1995-426571	19950421
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	US 1985-728834	B2	19850430		
	US 1985-744924	B2	19850614		
	US 1985-756814	B2	19850718		
	US 1986-821068	B2	19860121		
	US 1986-876819	B2	19860620		
	US 1986-923067	B2	19861024		
	US 1987-39654	B2	19870416		
	US 1987-39657	B1	19870416		
	US 1987-105261	B2	19871013		
	US 1991-799039	B2	19911127		
	US 1991-799411	B2	19911127		
	US 1987-99872	A2	19870922		
	EP 1987-309409	A	19871023		
	US 1988-157094	A3	19880209		
	US 1988-243253	B2	19880914		
	US 1989-358394	B1	19890526		
	US 1990-505256	B1	19900405		
	US 1991-794822	B1	19911118		
	US 1992-999280	A3	19921228		
	US 1993-24094	B1	19930226		
	US 1994-220454	A3	19940331		
	US 1995-401632	A3	19950309		

AB A colony stimulating factor, CSF-1, is a lymphokine useful in regulating the immune system is a lymphokine useful in overcoming the immunosuppression induced by chemotherapy or resulting from other causes. CSF-1 is obtained in usable amts. by recombinant methods, including cloning and expression of the murine and human DNA sequences encoding this protein. Both long and short forms of the human protein and muteins corresponding to the cDNA-encoded forms are disclosed. Thus, deletion of the first 3 N-terminal residues (Glu-Glu-Val) of mature CSF-1 (NV3) yields constructs that are expressed in Escherichia coli with ~95% of the N-terminal methionines removed. C-terminal truncated derivs. were also prep'd., with the new C-terminal residue at the 150, 190, 191, 221, 223, 236, 238, 249, 250, 258 or 411 positions. Muteins encoding an Asp at residue 59 (preferably via a GAT codon) do not show an internal restart translation product, thereby removing one cause of heterogeneity. Addnl. muteins can include substitution of lysine-52 with a glutamine residue, alteration of one or more glycosylation sites, and the cysteine-90 residue is dispensable to immunoreactivity. The CSF-1 proteins are capable both of stimulating monocyte-precursor/macrophage cell prodn. from progenitor cells, thus enhancing the effectiveness of the immune system, and of stimulating the functions of these differentiated cells as the secretion of lymphokines in the mature macrophages. They are also useful anti-infective agents, esp. as antiviral and antimicrobial agents.

IT 117277-07-3DP, N- and C-terminal truncated and substituted muteins
117277-09-5DP, N- and C-terminal truncated and substituted muteins
RE: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(nucleotide sequence; DNA encoding various truncated and mutein forms of human and murine colony stimulating factor-1)

PN 117277-07-3 CAPLUS
CN DNA, (mouse clone pcDBmuCSF-L colony-stimulating factor 1 cDNA plus flanks) (PCI) (CA INDEX NAME)

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STN Columbus

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RN 117277-09-5 CAPLUS

CN DNA, (mouse clone pcDBmuCSF-S colony-stimulating factor 1 cDNA plus
flanks) (9CI) (CA INDEX NAME)

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STN Columbus

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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
 DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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 * The CA role and document type information have been removed from *
 * the ED default display format and the ED field has been added, *
 * effective March 20, 2005. A new display format, IDERL, is now *
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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
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This file contains CAS Registry Numbers for easy and accurate substance identification.

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L18 ANSWER OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AT 1988-27967 CAPLUS

DN 12011953

TI A method for preparing a kit for the detection of antibodies to HCV (Hepatitis C virus) in biological samples such as blood serum

IN Houchens, Michael; Choo, Qui Lim; Kuo, George

PA Chiron Corp., India

SO Indian. 157 pp.

CODEN INXXAP

DT Patent

LA English

FAN.CNT 2

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JP 2733138	B2	19980330		
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ES 2134388	T3	19991001	ES 1995-114016	19910403
US 5682864	A	19971104	US 1992-910760	19920707
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LV 10344	B	19960220	LV 1993-4381	19930531
US 5679342	A	19971021	US 1993-97853	19930727
US 5350671	A	19940927	US 1993-103961	19930809
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HR 940493	B1	20001031	HR 1994-940493	19940907
US 5698390	A	19971216	US 1994-306472	19940915
US 6074816	A	20000613	US 1994-307273	19940916
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US 5712088	A	19980127	US 1995-440769	19950515
US 5096541	A	20000801	US 1995-441026	19950515
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US 2003162167	A1	20030828	US 1996-686983	19960725

STN Columbus

JP 09173079	A2	19970708	JP 1996-241451	19960822
JP 3171793	B2	20010604		
FI 9801380	A	19980615	FI 1998-1380	19980615
FI 106564	B1	20010228		
GR 3031361	T3	20000131	GR 1999-402455	19990929
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IN 1983-CA960	A	19881118		
US 1987-139886	A	19871230		
US 1988-161072	A	19880226		
US 1988-191263	A	19880506		
US 1988-263584	A	19881026		
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US 1989-325338	B2	19890317		
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US 1990-504352	A	19900404		
US 1990-505435	B2	19900404		
US 1990-566209	B1	19900808		
US 1990-611965	B2	19901108		
US 1991-US2225	A	19910329		
EP 1991-302910	A3	19910403		
US 1991-910760	A3	19920707		
US 1992-40564	A3	19930331		
US 1992-103961	A1	19930809		
US 1994-306472	A3	19940915		
US 1994-307273	A3	19940916		

AB: The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ -gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IN 155182-86-8

AL: PR2 (Properties)

(nucleotide sequence of)

EN 155182-86-8 CAPLUS

CS BFA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

SEQ 1 ctggctgcgt ggtcatagtg ggcagggtcg tcttgccgg gaagccggca
51 atcatacctg acaggaagt cctctaccga gagttcgatg agatggaaga

STN Columbus

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L18 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1988:32855 CAPLUS

DN 108:32855

TI Nucleotide sequence, promoter analysis, and linkage mapping of the unusually organized operon encoding ribosomal proteins S7 and S12 in maize chloroplast

AU Giese, Klaus; Subramanian, Alap R.; Larrinua, Ignacio M.; Bogorad, Lawrence

CS Abt. Wittmann, Max-Planck-Inst. Mol. Genet., Berlin, D-1000/33, Fed. Rep. Ger.

SO Journal of Biological Chemistry (1987), 262(31), 15251-5

====

CODEN: JBCHA3; ISSN: 0021-9258

DT Journal

LA English

AB The nucleotide sequence of the operon encoding maize chloroplast ribosomal protein genes S7 and S12 and the promoter activity of a chimeric construct of the -10/-35 sequence of this operon (attached to a promoterless chloramphenicol acetyltransferase gene) were detd. This operon occurs in the chloroplast genome divided in 2 parts: part A contains exon 1 or rpS12 (encoding the N-terminal 38 amino acid residues), whereas part B has the following structure: promoter-rpS12 (exon 2 + intron + exon 3)-spacer-rpS7-terminator. Part A is located at the approx. coordinate position 41,000, whereas 2 copies of part B are located at 2 distant locations in the genome at coordinate positions 18,700 and 120,200. This unusual organization of the S12 operon in maize (a monocot plant) is similar to that reported in a dicot and a lower plant. The deduced amino acid sequence of maize chloroplast S7 shows 43, 38, 71, and 85% and of S12 shows 66, 72, 91 and 90% sequence identity to the corresponding sequences of *Escherichia coli*, *Euglena gracilis*, *Marchantia polymorpha*, and *Nicotiana tabacum*, resp. The promoter upstream of rpS12 (part B) is transcriptionally active in *E. coli*.

IT 112263-07-7

RL: P&P (Properties); BIOL (Biological study)

(nucleotide sequence of)

RN 112263-07-7 CAPLUS

CN DNA (corn chloroplast gene rps12 coding region) (9CI) (CA INDEX NAME)

NTE doublestranded

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SEQ      1 atgcctacta ttcaacaatt aattagaaat aaaagacaac ccatcgaaaa
      51 tagaagaaaa tcaccagccc tttaaaggatg ccttcaacgt agaggagtat
     101 gtactagagt gtatactatc aacccccaaa aacccaactc tgccttacgt
     151 aaagttgccg gactacgatt aacctctgga ttgaaatca ctgcttatat
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STN Columbus

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CA SUBSCRIBER PRICE	-1.46	-5.11

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 DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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 * effective March 20, 2005. A new display format, IDERL, is now *
 * available and contains the CA role and document type information. *
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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
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STN Columbus

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FILE COVERS 1997 - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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L25 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS

DN 120:296653

TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum

IN Houghton, Michael; Choo, Qui Lim; Kuo, George

PA Chiron Corp., India

SO Indian: 157 pp.

CODEN: INXXAP

DT Patent

LA English

FAN: CNT 8

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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STN Columbus

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US 2003162167	A1	20030828	US 1996-686983	19960725
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JP 3171793	B2	20010604		
FI 9801380	A	19980615	FI 1998-1380	19980615
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GR 3031361	T3	20000131	GR 1999-402455	19990929
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IN 1988-CA960	A	19881118		
US 1987-139886	A	19871230		
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US 1988-191263	A	19880506		
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US 1988-271450	A	19881114		
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JP 1992-361785	A3	19881118		
JP 1992-361787	A3	19881118		
JP 1993-178446	A3	19881118		
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JP 1998-111631	A3	19881118		
WO 1988-US4125	A	19881118		
YU 1988-2138	A6	19881118		
US 1989-325338	B2	19890317		
US 1989-341334	B2	19890420		
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NO 1989-2931	A	19890717		
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WO 1991-US2225	A	19910329		
EP 1991-302910	A3	19910403		
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US 1993-40564	A3	19930331		
US 1993-103961	A1	19930809		
US 1994-306472	A3	19940915		
US 1994-307273	A3	19940916		
AB	The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA			

STN Columbus

suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ -gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-86-8

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

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=> file registry

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

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246.11

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

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TOTAL

ENTRY

SESSION

CA SUBSCRIBER PRICE

-0.73

-5.84

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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*
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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

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 information enter HELP PROP at an arrow prompt in the file or refer
 to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

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CA SUBSCRIBER PRICE	0.00	-5.84

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate
 substance identification.

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STN Columbus

=> d bib ab hitseq 1-3

L30 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS

DN 120:296653

TI A method for preparing a kit for the detection of antibodies to HCV
(hepatitis C virus) in biological samples such as blood serum

IN Houghton, Michael; Choo, Qui Lim; Kuo, George

PA Chiron Corp., India

SC Indian, 157 pp.

CODEN: INXXAP

DT Patent

LA English

FAN.CNT 3

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	HU 62706	A2	19930528	HU 1992-3146	19910329
	HU 217025	B	19991129		
	JP 05508219	T2	19931118	JP 1991-507636	19910329
	JP 2753138	B2	19980330		
	RO 109916	B1	19950728	RO 1975-92012	19910329
	PL 172133	B1	19970829	PL 1991-296329	19910329
	RU 2130969	C1	19990527	RU 1991-5053084	19910329
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STN Columbus

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JP 1996-241451	A3	19881118		
JP 1998-111631	A3	19881118		
WO 1983-US4125	A	19881118		
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STN Columbus

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WO 1991-US2225	A	19910329
EP 1991-302910	A3	19910403
US 1992-910760	A3	19920707
US 1993-40564	A3	19930331
US 1993-103961	A1	19930809
US 1994-306472	A3	19940915
US 1994-307273	A3	19940916

AB The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunocassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ -gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-96-8

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-96-8 CAPLUS

CN DNA (Hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(961) (CA INDEX NAME)

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SEQ      1  atggcctgcgt ggtcatagtg ggcagggtcg tcttgccgg gaagccggca
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          101  ggtctctcag cacttacgtg acatcgagca agggatgatg ctgcccggagc
          151  ggttcaagca gaaggccctc ggctcctgc agaccgcgtc ccgtcaggca
          201  gaggttatcg cccctgctgt ccagaccaac tggcaaaaac tgcgacctt
          251  atggggcgaag catatgtgga acttcatcag tgggatacaa tacttggcgg
          301  gcttgctcaac gctgctggt aaccccgcca ttgcttcatt gatggctttt
          351  acagctgctg tcaccagccc actaaccact agccaaa

```

L30 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1996:54/329 CAPLUS

DN 105:147329

TI A genetically engineered murine/human chimeric antibody retains
specificity for human tumor-associated antigen

AU Sahagun, Barbara G.; Dorai, Haimanti; Saltzgaber-Muller, Jo; Toneguzzo,
Francesco; Guindon, Cathy A.; Lilly, Sarah P.; McDonald, Kevin W.;
Morrissey, David V.; Stone, Barry A.; et al.

CS New Technol. Res., E. I. DuPont de Nemours and Co., Billerica, MA; 01862;
USA

SO Journal of Immunology (1986), 137(3). 1066-74

====
CODEN: JOIMA3; ISSN: 0022-1767

DT Journal

LA English

OS CASREACT 105:147329

AB Chimeric immunoglobulin genes were constructed by fusing murine variable

STN Columbus

region exons to human const. region exons. The ultimate goal was to produce an antibody capable of escaping surveillance by the human immune system while retaining the tumor specificity of a murine monoclonal. The murine variable regions were isolated from the functionally expressed κ and γ 1 immunoglobulin genes of the murine hybridoma cell line B6.2, the secreted monoclonal antibody of which reacts with a surface antigen from human breast, lung, and colon carcinomas. The κ and γ 1 chain fusion genes were cointroduced into non-antibody producing murine myeloma cells by electroporation. Transfectants that produced murine/human chimeric antibody were obtained at high frequency, as indicated by immunoblots probed with an antisera specific for human Ig. Enzyme-linked immunoabsorbent assay anal. demonstrated that this chimeric antibody was secreted from the myeloma cells and retained the ability to bind selectively to membrane prepd. from human tumor cells. The chimeric Ig was also shown by indirect fluorescence microscopy to bind to intact human carcinoma cells with the specificity expected of B6.2. The ability of chimeric antibody to recognize human tumor-assocd. antigen makes feasible a novel approach to cancer immunotherapy.

IT 104491-32-9

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 104491-32-9 CAPLUS

CN DNA (mouse clone pSV2gpt/B6.2VLhuCk B6.2 immunoglobulin G 1
 κ -chain fragment-specifying) (9CI) (CA INDEX NAME)

NTE doublestranded

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SEQ      1 gacattgtga tgaccagtc tcaaaaattc atgtccacat cagtgggaga
      51 cagggtcagc gtcacctgca aggccagtca gaatgtggtc actaatgtag
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     301 gggaccaagc tggagctgaa acgg
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L30 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:18693 CAPLUS

DN 102:18693

TI Characterization of three chicken pseudogenes for U1 RNA

AU Kristo, Paula; Tsai, Ming Jer; O'Malley, Bert W.

CS Dep. Cell Biol., Baylor Coll. Med., Houston, TX, 77030, USA

SO DNA (1984), 3(4), 281-6

CODEN: DNAADR; ISSN: 0193-0238

DT Journal

LA English

AB Three chicken genomic DNA clones contg. the U1 RNA sequence were isolated from a chicken gene library and characterized. Two of these clones, CL64, and CL111, are overlapping clones which show several single-nucleotide changes in the U1 coding sequence, suggesting that they probably are alleles of the same sequence. The U1 sequence in the 3rd clone, CL40, is more divergent. Flanking regions of these genes do not share any sequence homol. between each other or with the previously isolated chicken genomic clone CL59. A short repeat CGGGG appears 28 times upstream of the U1 sequence in CL59. Another repeat, GCACC, is repeated 14 times upstream of the U1 region in CL40.

IT 93927-63-0

RL: PRP (Properties)

STN Columbus

(characterization and sequence for)
 PN 93927-63-0 CAPLUS
 CN DNA (chicken clone CL40 U1 RNA pseudogene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 ttaccttgac ccgcctgagg tttttccatt gctctgggca ggaggatgtt
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 101 gagaactttg gacttcactt taatcccaca tcagtggggg ttggacgagg
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CA SUBSCRIBER PRICE		

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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
 DICTIONARY FILE UPDATES: 23 APR 2005 HIGHEST RN 849459-72-9

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 *
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 * the IDS default display format and the ED field has been added, *
 * effective March 20, 2005. A new display format, IDERL, is now *
 * available and contains the CA role and document type information. *
 *

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
 information enter HELP PROP at an arrow prompt in the file or refer
 to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s tgctgtccag/sqen
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STN Columbus

(TGCTGTCCAG/SQEN AND SQL=10)

=> s tgctgtccag/sqsn
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=> s l32 and SQL<400
22713436 SQL<400
L33 6562 L32 AND SQL<400

=> file caplus		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
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	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	-8.03

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FILE COVERED 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

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L35 1 L34 AND PY<1990

=> d bib ab hitseq

L35 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text:

AN 1994:296653 CAPLUS

DN 120:296653

TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum

IN Houghton, Michael; Choo, Qui Lim; Kuo, George

PA Chiron Corp., India

SO Indian, 157 pp.

CODEN: INXXAP

DT Patent

STN Columbus

LA English

FAN.CNT 8

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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	IN 171240	A	19920822	IN 1990-CA808	19900917
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	JP 2733138	B2	19980330		
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WO 1989-US4125	A	19881118		
YU 1988-2138	A6	19881118		
US 1989-325338	B2	19890317		
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US 1990-505435	B2	19900404		
US 1990-566209	B1	19900808		
US 1990-611965	B2	19901108		
WO 1991-US2225	A	19910329		
EP 1991-302910	A3	19910403		
US 1992-910760	A3	19920707		
US 1993-40564	A3	19930331		
US 1993-103961	A1	19930809		
US 1994-306472	A3	19940915		
US 1994-307273	A3	19940916		

AB: The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also

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provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ -gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in *Escherichia coli* as fusion products with superoxide dismutase.

IT 155182-86-8

RL: PRP (Properties)

(nucleotide sequence of)

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

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=> File Registry

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FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

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 DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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 *
 * The CA roles and document type information have been removed from *

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* the IDE default display format and the ED field has been added, *
 * effective March 20, 2005. A new display format, IDERL, is now *
 * available and contains the CA role and document type information. *
 *

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
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This file contains CAS Registry Numbers for easy and accurate substance identification.

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STN Columbus

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L40 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS
 DN 120:296653
 TI A method for preparing a kit for the detection of antibodies to HCV
 (hepatitis C virus) in biological samples such as blood serum
 IN Houghton, Michael; Choo, Qui Lim; Kuo, George
 PA Chiron Corp., India
 SO Indian, 157 pp.
 CODEN: INXXAP
 DT Patent
 LA English
 FAN.CNT 8

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WO 1991-US2225	A	19910329
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US 1992-910760	A3	19920707
US 1993-40564	A3	19930331
US 1993-103961	A1	19930809
US 1994-306472	A3	19940915
US 1994-307273	A3	19940916

AB The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ -gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-84-6, DNA (hepatitis C virus clone 5-1-1 cDNA)
155182-86-8 155182-87-9, DNA (hepatitis C virus clone 5-1-1 cDNA)

PL: PNP (Properties)
(nucleotide sequence of)

RN 155182-84-6 CAPLUS

CN DNA (hepatitis C virus clone 5-1-1 polyprotein fragment-specifying) (9CI)
(CA INDEX NAME)

SEQ 1 ggctctctgc ttgaactgct cggcgagcat cttacctgac agggaagtcc
51 tctaccgaga gtctgatgag atggaagagt gctctcagca cttaccgtac
101 atcgagcaag ggatgatgct cggcgagcag ttcaagcaga aggccctcgg
151 cctcc

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

SEQ 1 ctggctgctg ggtcatagtg ggcagggtcg tcttgtccgg gaagccggca
51 atcatacctg acagggaagt cttctaccga gagttcgatg agatggaaga
101 gtgctctcag cacttaccgt acatcgagca agggatgatg ctgcgcgagc
151 agttcaagca gaaggccctc ggctctctgc agaccgcgtc ccgtcaggca
201 gaggttatcg cccctgctgt ccagaccaac tggcaaaaac tcgagacctt
251 ctgggcgaag catatggya acttcatcag tgggatataa tacttggcgg
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351 acagctgctg tcaccagccc actaaccact agccaaa

RN 155182-87-9 CAPLUS

STN Columbus

CN DNA (hepatitis C virus clone 1-2 164-nucleotide fragment) (9CI) (CA INDEX NAME)

SEQ 1 ggcatagtg ggcagggtcg tcttgccgg gaagccggca atcatacctg
51 acaggggaagt cctctatcga gagttcgatg agatggaaga gtgctctcag
101 cacttaccgt acatcgagca agggatgatg ctgcccagc agttcaagca
151 gaaggccctc ggcc

L40 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:230854 CAPLUS

DN 112:230854

TI Synthetic gene encoding human interleukin 5

IN Edwards, Richard Mark

PA British Bio-Technology Ltd., UK

SO Brit. UK Pat. Appl., 21 pp.

CODEN: BAXXDU

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	GB 2217328	A1	19891025	GB 1988-8524	19880412 <--
	GB 2217328	B2	19920129		
PEAI	GB 1988-8524		19880412		

AB A synthetic gene encoding human interleukin-5 is described. The gene contains restriction sites at frequent intervals to facilitate cassette transfection. The gene also is flanked by restriction sites which simplifies its incorporation into desired expression systems. The gene was cloned in Escherichia coli.

IN 127314-99-2

AD: PEP (Properties)

(nucleotide sequence of and cloning in Escherichia coli of)

RE 127314-99-2 CAPLUS

CN DNA, (human clone ph-IL-5-30 interleukin 5 [Met-1]-specifying plus flanks) (9CI) (CA INDEX NAME)

SEQ 1 agcttacct gccatggaaa ttcccactag tgcattggtg aaagagacct
51 tggcactgct ttctactcat cgaactctgc tgatagccaa tgagactctc
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201 tggaaagact attcaaaaac ttgtccttaa taagaaata catcgatggc
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> File registry

COST IN U.S. DOLLARS

FULL ESTIMATED COST

SINCE FILE

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18.24

TOTAL

SESSION

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DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE

ENTRY

TOTAL

SESSION

STN Columbus

CA SUBSCRIBER PRICE

-1.46

-10.22

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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conducting SmartSELECT searches.

*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.acs.org/CHLINE/DBSS/registryss.html>

```
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      0 GGCCTCCTGC/SQEN
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L41 0 GGCCTCCTGC/SQEN
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=> s ggcctcctgc/sqsn and SQL<400
SYSTEM LIMITS EXCEEDED - SEARCH ENDED
The search profile you entered was too complex or gave too many
answers. Simplify or subdivide the query and try again. If you have
exceeded the answer limit, enter DELETE HISTORY at an arrow prompt
(=>) to remove all previous answers sets and begin at L1. Use the
SAVE command to store any important profiles or answer sets before
using DELETE HISTORY.
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=> s ggcctcctgc/sqsn
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L43 3074 L42 AND SQL<400
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=> file coplus
COST IN U.S. DOLLARS

FULL ESTIMATED COST
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STN Columbus

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

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=> S L4 AND PY<1990
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=> d bdb ab hitseq 1 2

L45 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 19941236653 CAPLUS

DN 1201298653

TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum

IN Houghton, Michael; Choo, Qui Lim; Kuo, George

PA Chiron Corp., India

SO Immunol. 157 pp.

CODEN INXXAP

DT Patent

LA English

FAN CNF 8

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STN Columbus

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US 1994-306472	A3	19940915		
US 1994-307273	A3	19940916		

AB The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ -gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-86-5, DNA (hepatitis C virus clone 5-1-1 cDNA)

155182-86-8

STN Columbus

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-84-6 CAPLUS
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(CA INDEX NAME)

SEQ 1 ggccctcctgc ttgaactgct cggcgagcat catacctgac agggaagtcc
51 tctaccgaga gttcgatgag atggaagagt gctctcagca cttaccgtac
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151 cctcc

RN 155182-86-8 CAPLUS
CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

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L45 155182-84-6 CAPLUS COPYRIGHT 2005 ACS on STN

ENGLISH

RN 155182-86-8 CAPLUS

DT 104245-22

TE Genes for tRNA and their putative expression signals in *Methanococcus*

AB Rich, Guenter; Sibold, Lionel; Boeck, August

CS Univ. Muenchen, Munich, 8000/19, Fed. Rep. Ger.

SO Systematic and Applied Microbiology (1986), 7(1), 18-25

====

CODEN: SAMIDF; ISSN: 0723-2020

DT Journal

LA English

AB A no. of tRNA genes from *M. vannielii* were cloned and sequenced. They belong to 6 putative transcriptional units comprising 11 tRNA genes. Together with the tRNA gene sequences previously reported, this brings the total of *Methanococcus* tRNA genes now analyzed to 19, organized in 7 putative transcriptional units. In 2 of the tRNA gene clusters (one comprising 2 genes, the other, 6 genes) one of the genes possesses opposite transcriptional polarity and is sepd. from the remaining gene(s) by a spacer of 146 and 115 nucleotides, resp. Comparison of the region flanking the 7 transcriptional units at the 5' end yielded a consensus sequence between -25 and -50 bases upstream. In the tRNA gene clusters with opposite transcriptional polarity this sequence occurred twice and also in inverse polarity. This observation and the fact that this sequence was the only detectable motif of homologous primary structures in 5'-upstream regions of tRNA genes indicates that it may be involved in transcription initiation. Common motifs at the 3'-flanking regions, which may possibly be involved in transcription termination, are also presented.

IT 104245-31-0

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

STN Columbus

RN 104245-31-0 CAPLUS
CN DNA (Methanococcus vannielii tRNAThr GGU gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 agcctcaggc ggggtttgaa cccgcggcct cctgcttacc aagcaggcgc
51 tctaccaggc tgagccactg aggc

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FULL ESTIMATED COST		
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CA SUBSCRIBER PRICE		

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STN Columbus

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COST IN U.S. DOLLARS

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FULL ESTIMATED COST

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FILE COVERS: 107 - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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L49 278 L48

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L50 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 2004:286653 CAPLUS

DN 12066511

TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum

IN Houghton, Michael; Choo, Qui Lim; Kuò, George

PA Chiron Corp., India

SO Indochina 157 pp.

CODEN INXXAP

DT Patent

LA English

FAN: CHT 8

PATENT NO.

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APPLICATION NO.

DATE

STN Columbus

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STN Columbus

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45. The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV

STN Columbus

epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ -gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-86-8

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

SEQ 1 ctggctgcgt ggtcatagt ggcagggtcg tcttgctcgg gaagccggca
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151 agttcaagca gaagggccctc ggctctctgc agaccgcgtc ccgtcaggca
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File Registry
COST U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
9.84	531.01

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL
ENTRY	SESSION
-0.73	-12.41

CA SUBSCRIBER PRICE

FILE REGISTRY ENTERED AT 16:12:10 ON 29 APR 2005
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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

Please note that search-term pricing does apply when conducting SmartSELECT searches.

* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *

STN Columbus

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

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COST IN U.S. DOLLARS	40.24	571.25
FULL ESTIMATED COST		

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FILE "HELP US" ENTERED AT 16:13:55 ON 29 APR 2005
 USE TO AGREE TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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FILE CHGVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

New CAS Information Use Policies. enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

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STN Columbus

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L55 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS

DN 120:296653

TI A method for preparing a kit for the detection of antibodies to HCV
(hepatitis C virus) in biological samples such as blood serum

IN Houghton, Michael; Choo, Qui Lim; Kuo, George

PA Chiron Corp., India

SO Indian, 157 pp.

CODEN: INXXAP

DT Patent

LA English

FAN.CNT: 8

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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STN Columbus

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GB 1987-139826	A	19871230		
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US 1987-325333	B2	19890317		
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US 1989-353896	B2	19890421		
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US 1989-355961	B2	19890518		
NO 1989-2931	A	19890717		
US 1989-398667	B2	19890825		

STN Columbus

US 1989-456637	B2	19891221
US 1990-504352	A	19900404
US 1990-505435	B2	19900404
US 1990-566209	B1	19900808
US 1990-611965	B2	19901108
WO 1991-US2225	A	19910329
EP 1991-302910	A3	19910403
US 1992-910760	A3	19920707
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US 1993-103961	A1	19930809
US 1994-306472	A3	19940915
US 1994-307273	A3	19940916

=> s ctggctgc/sqen

REGISTRY INITIATED

Substance data SEARCH and crossover from CAS REGISTRY in progress...
 Use DISPLAY HITSTR (or FHITSTR) to directly view retrieved structures.

L57

O L56

=> file registry

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

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DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE

TOTAL

ENTRY

SESSION

CA SUBSCRIBER PRICE

0.00

-12.41

FILE 'REGISTRY' ENTERED AT 16:16:01 ON 29 APR 2005

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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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 *
 * The CA roles and document type information have been removed from *
 * the IDE default display format and the ED field has been added. *
 * effective March 20, 2005. A new display format, IDERL, is now *
 * available and contains the CA role and document type information. *
 *

STN Columbus

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Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

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=> s 158 and SQL<400
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=> file caplus		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	32.96	616.23
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	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	-12.41

FILE 'CAPLUS' ENTERED AT 16:17:28 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s 150
 L60 6350 L50

=> s 160 and PY<1990
 13008711 PY<1990
 L61 62 L60 AND PY<1990

=> d bib ab hitseq 1-52

L61 ANSWER 1 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:597650 CAPLUS

DE 121:197650

TI Method for HLA DP typing

IN Erlich, Henry A.; Horn, Glenn T.; Bugawan, Teodorica; Begovich, Ann B.

STN Columbus

PA Hoffmann-La Roche, Inc., USA
 SO U.S., 22 pp. Cont.--in-part of U.S. Ser. No. 258,212, abandoned.
 CODEN: USXXAM
 DT Patent
 LA English
 FAN.CNT 27

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5310893	A	19940510	US 1989-347506	19890504
	WO 8911547	A1	19891130	WO 1989-US2169	19890518 <--
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	AU 633830	B2	19930211		
	EP 417160	A1	19910320	EP 1989-906241	19890518
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	JP 3117083	B2	20001211		
	AT 140035	E	19960715	AT 1989-906241	19890518
	IL 90357	A1	19930818	IL 1989-90357	19890519
	CA 1339206	A1	19970805	CA 1989-600226	19890519
	US 5541065	A	19960730	US 1994-195615	19940214
	JP 10155500	A2	19980616	JP 1997-281834	19971015
	JP 3070837	B2	20000731		
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	US 1989-893331	B2	19860331		
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	US 1989-839331	A2	19860313		
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	US 1989-281834	A3	19870313		
	US 1989-347506	A	19890504		
	WO 1989-US2169	A	19890518		

AB A process for detg. the genotype of an individual with respect to the alleles at the HLA DP locus involves obtaining a sample of nucleic acid from the individual, and hybridizing the nucleic acids with a panel of probes specific for variant segments of DP α and DP β genes. Because the variation between DP β alleles is highly dispersed throughout the second exon of the DP β gene, the discovery of many different DP β alleles makes the process far more discriminating and informative than cellular RFLP, or seral methods. The process can also be carried out on amplified nucleic acid produced by the polymerase chain reaction using primers specific for the second exon of the DP α and DP β genes. HLA DP DNA typing methods are useful in the prevention of graft rejection and host vs. graft disease, in detg. susceptibility to autoimmune diseases, in providing evidence concerning the derivation from an individual of forensic samples, and in paternity testing.

INT 150052-04-3

RL USGS (Uses)

(primer, for amplification of HLA DP α locus)

RN 150052-04-3 CAPLUS

CN AGA, GAC-T-G-G-C-T-G-C-A-G-T-G-T-G-G-T-T-G-G-A-A-C-G-C) (9CI) (CA INDEX NAME)

NTE singlestranded

SEQ 1 ctggctgcag tctggttgga acgc

STN Columbus

L61 ANSWER 2 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS

DN 120:296653

TI A method for preparing a kit for the detection of antibodies to HCV
(hepatitis C virus) in biological samples such as blood serum

IN Houghton, Michael; Choo, Qui Lim; Kuo, George

PA Chiron Corp., India

SO Indian, 157 pp.

CODEN: INXXAP

DT Patent

LA English

FAN CNF 8

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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STN Columbus

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US 1988-191263	A	19880506		
US 1988-263584	A	19881026		
US 1988-271450	A	19881114		
CN 1988-107988	A	19881118		
JP 1988-361785	A3	19881118		
JP 1988-361787	A3	19881118		
JP 1988-178446	A3	19881118		
JP 1988-241451	A3	19881118		
JP 1988-111631	A3	19881118		
NO 1988-US4125	A	19881118		
US 1988-2138	A6	19881118		
US 1989-325338	B2	19890317		
US 1989-341334	B2	19890420		
US 1989-353896	B2	19890421		
US 1989-355002	B2	19890518		
US 1989-355961	B2	19890518		
NO 1989-2931	A	19890717		

STN Columbus

US 1989-398667	B2	19890825
US 1989-456637	B2	19891221
US 1990-504352	A	19900404
US 1990-505435	B2	19900404
US 1990-566209	B1	19900808
US 1990-611965	B2	19901108
WO 1991-US2225	A	19910329
EP 1991-302910	A3	19910403
US 1992-910760	A3	19920707
US 1993-40564	A3	19930331
US 1993-103961	A1	19930809
US 1994-306472	A3	19940915
US 1994-307273	A3	19940916

AB The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ -gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in *Escherichia coli* as fusion products with superoxide dismutase.

IT 155182-36-8

RL: PRP (Properties)

(nucleotide sequence of)

RI 155182-36-8 CAPLUS

CS HCV (Hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(CC) (CA INDEX NAME)

SEQ
 51 accatacctg acaggaagt cctctaccga gagttcgatg agatggaaga
 101 gtgctctcag cacttacctg acatcgagca agggatgatg ctcqccgagc
 151 gctcaagca gaaggccctc ggctctctgc agaccgcgtc ccgtcaggca
 201 gaggctatcg cccctgctgt ccagatcaac tggcaaaaac tcgagacctt
 251 cggggcggaag catatgtgga acctcatcag tgggatacaa tacttgccgg
 301 gcttgctcaac gctgcctggt aaccccgcca ttgcttcatt gatggctttt
 351 agctgctg tcaccagcgg actaaccact agccaaa

L61 ANSWER 1 OF 62. CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1591-14088 CAPLUS

DN 114:179080

TI Cloning and analysis of the gene for the major outer membrane lipoprotein from *Pseudomonas aeruginosa*

AU Cornellis, P.; Bouia, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Humbert, V.; Hubert, J. C.

CS Lab. A. Microbiol., Univ. Louis Pasteur, Strasbourg, 67070, Fr.

SO Molecular Microbiology (1989), 3(3), 421-8

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CODEN: MOMIEE; ISSN: 0950-382X

DT Journal

LA English

AB The gene for the *P. aeruginosa* outer membrane lipoprotein I was isolated from a genomic library in the phage λ EMBL3 vector and subsequently

STN Columbus

subcloned in the low copy-no., wide host-range plasmid vector, pKT240. The cloned gene was highly expressed, resulting in the prodn. of a low mol.-wt. protein (8 kD) that was found to be assocd. with the outer membrane. Sequence anal. showed an open reading frame of 83 amino acids with a putative N-terminal hydrophobic signal peptide of 19 residues immediately followed by the lipoprotein consensus sequence, GLY-CYS-SER-SER (residues 19-22). The predicted amino acid compn. of the mature polypeptide and that of the purified lipoprotein I of *P. aeruginosa* were identical. In contrast with other Gram-neg. outer membrane lipoproteins, conformation predictions suggested that the mature protein was a single alpha helix.

IT 133020-34-5, Deoxyribonucleic acid (*Pseudomonas aeruginosa* clone pLPI lipoprotein Opr I gene)
 RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)
 RN 133020-34-5 CAPLUS
 CN DNA (*Pseudomonas aeruginosa* clone pLPI lipoprotein Opr I gene) (9CI) (CA INDEX NAME)

SEQ 1 atgaacaacg ttctgaaatt ctctgctctg gctctggctg ctgttctggc
 51 caccgggttg agcagccact ccaagaaac cgaagctcgt ctgaccgcta
 101 ccgaagacgc agctgctcgt gctcaggctc gcgctgacga agcctatcgc
 151 aaggctgacg aagctctggg cgctgctcag aaagctcagc agaccgctga
 201 cgaggctaac gagcgtgccc tgcgcatgct ggaaaaagcc agccgcaagt
 251 aatag

ALL RIGHTS OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

FILE NAME

AU 133020-34-5 CAPLUS

CA 133020-34-5

TI Cloning of gene for natriuretic and vasodilator peptide and its use for recombinant manufacture of these peptides

TV Seifrieder, J.; Jeffrey, Lewicki, John; Scarborough, Robert M.; Porter, J. Gordon

PA California Biotechnology, Inc., USA

SC PCT Int. Appl., 61 pp.

CODEN PIXXD2

DT Patent

LA English

PAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 8912069	A1	19891214	WO 1989-US2373	19890531
W: AU, JP, KR, US				
RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
CA 1339210	A1	19970305	CA 1989-601005	19890529
AU 8937681	A1	19900105	AU 1989-37681	19890531
EP 418308	A1	19910327	EP 1989-906935	19890531
EP 418308	A1	19950816		
R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
JP 03505280	B2	19911121	JP 1989-506595	19890531
JP 2511160	B2	19960626		
US 5114923	A	19920519	US 1990-460855	19900202
US 5674710	A	19971007	US 1990-477226	19900208
US 5948761	A	19990907	US 1997-850910	19970505
US 6586396	B1	20030701	US 1999-287892	19990407
US 2003109430	A1	20030612	US 2001-902517	20010709
US 2004002458	A1	20040101	US 2003-402021	20030327

STN Columbus

PRAI US 1988-200383 A 19880531
 US 1988-206470 A 19880614
 US 1989-299880 A2 19890119
 WO 1989-US2373 A 19890531
 US 1990-460855 A 19900202
 US 1990-477226 A3 19900208
 US 1997-850910 A3 19970505
 US 1999-287892 A3 19990407

OS MARPAT 114:158509

AB The cDNA encoding prepro natriuretic peptide (NP) of porcine brain is cloned, sequenced, and used to clone the gene encoding natriuretic related peptide (NRP) from the genomic DNA of, e.g. pig, rat. From a porcine heart tissue cDNA library, an unprocessed cDNA encoding porcine brain natriuretic peptide (PBNP) was cloned and sequenced. The cDNA clone (clone 14) contained at least an intron at residue Val22 of the 26-amino acid BNP (brain natriuretic peptide) and an upstream intron. Using clone 14 as a probe, the canine NRP-encoding gene was cloned and subcloned into plasmid pBR322 to obtain plasmid pDBNP-1, which was subsequently used to clone the human NRP gene.

IT 132444-45-2 132444-46-3 132444-48-5

RL: PRP (Properties)

(cloning of cDNA for and nucleotide sequence of)

RN 132444-45-2 CAPLUS

CN DNA, (swine brain natriuretic peptide-26 [Gly-9Ile-8Arg-7Ser-6Pro-5Lys-4Thr-3Met-2Arg-1]-specifying) (9CI) (CA INDEX NAME)

STRUCTURE DIAGRAM IS NOT AVAILABLE

RN 132444-46-3 CAPLUS

CN DNA, (swine brain natriuretic peptide-26 [Ser-6Pro-5Lys-4Thr-3Met-2Arg-1]-specifying) (9CI) (CA INDEX NAME)

STRUCTURE DIAGRAM IS NOT AVAILABLE

RN 132444-48-5 CAPLUS

CN DNA, (swine brain natriuretic peptide-26 [Thr-3Met-2Arg-1]-specifying) (9CI) (CA INDEX NAME)

STRUCTURE DIAGRAM IS NOT AVAILABLE

IT 132606-95-5, Deoxyribonucleic acid (pig brain natriuretic factor messenger RNA-complementary) 132444-47-4; Deoxyribonucleic acid (pig brain natriuretic factor-26-specifying)

RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence and cloning of)

RN 132606-95-5 CAPLUS

CN DNA (swine brain natriuretic peptide cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgggcccc ggatggcgtt tccccgggtg ctctgtctcc tgttcttga
 51 cctgttgctg ctaggatgcc gttcccatcc actgggtggc gctggcctgg
 101 cctcagaact gccagggata caggaggtgc ggaaccgct gcgagacagg
 151 gtctccgagc tgcaggcggg gcggacggac ctggagcccc tccggcagga
 201 ccgtggcctc acagaagcct gggaggcgag ggaagcagcc cccacggggg
 251 ttcttgggcc ccgcagtagc tatcttccaag tctccgggg aatacgcagc
 301 cccaagacga tgcctgaact tggctgcttt gggcggaggc tggaccggat
 351 cggctccctc agcggcctgg gctgcaatgt gctcaggagg tactga

RN 132444-47-4 CAPLUS

CN DNA (swine brain natriuretic peptide-26-specifying) (9CI) (CA INDEX NAME)

NTE doublestranded

STN Columbus

SEQ 1 gactctggct gctttgggcg gaggtctggac cggatcggct ccctcagcgg
51 cctgggctgc aatgtgctca ggaggtactg a

L61 ANSWER 5 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:494354 CAPLUS

DN 113:94354

TI Amyloid protein precursors, genetic probes, antibodies, and their use in diagnosis of Down's syndrome and Alzheimer's disease

IN Neve, Rachael L.

PA Children's Medical Center Corp., USA

SO PCT Int. Appl., 33 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 8907657	A1	19890824	WO 1989-US549	19890210 <---
	W: AU, BR, DK, JP, KR				
	RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
	AU 8922046	A1	19890906	AU 1989-32046	19890210 <---
PRAI	US 1988-154236	A	19880210		
	WO 1989-US549	A	19890210		

AB A form of amyloid β -protein precursor DNA (designated APP-1) on chromosome 21 contains an exon encoding a polypeptide sharing significant homology with Kunitz-type serine protease inhibitors. An alternate form (designated APP-2) lacks this exon, is expressed only in the brain, and has a pattern of distribution parallel to that of amyloid deposits in brains of patients with Alzheimer's disease and Down's syndrome. The exon is inserted at base pair 365 of APP-1 and interrupts the Val-289 codon of APP-1, changing it to an ile codon. The 2 forms, or their corresponding cDNAs, are distinguished for diagnosis of the above diseases by selective hybridization, using a probe contg. the APP-2 Val-289 codon and subsequents on either side that hybridize to APP-2 nucleic acid but are too short to hybridize to APP-1 nucleic acid, and another probe contg. a sequence from the APP-1 exon long enough to hybridize to APP-1 nucleic acid. The corresponding polypeptides, contg. or not contg. the exon-encoded sequence, can be detected by use of specific antibodies for diagnosis of these diseases. The course of Alzheimer's disease and Down's syndrome involves a general decrease of APP-2 expression in affected areas of the brain, but a substantial increase in APP-1 expression in brain and peripheral tissue. Thus, a cDNA library was constructed from mRNA of human promyelocytic leukemia cell line HL60 and screened with FB68L, a fetal brain cDNA corresponding to the 3' portion of the APP gene, for probe selection. In a 19-wk Down's syndrome fetal brain, the hybridization of probes AMY3 (5'-CTGGCTGCTGTTGTAGGAACCTCGAACCACCTTCCACAGA-3') and HL1241 (5'-TATGCAGTACTCTTCTGTGTCA-3') was greater than that to normal 19-wk fetal brain, indicating elevated levels of APP mRNA. In frontal cortex of Alzheimer's disease patients, expression of mRNA hybridizing to HL1241 (i.e. contg. the exon-encoded sequence) was near normal, whereas that of mRNA hybridizing to AMY3 was markedly diminished.

IP 129750 91-2

RL ABST (Analytical study)

Amyloid protein precursor 2 detection by hybridization with)

RM 129750-91-2 CAPLUS

CM DNA d(C-T-G-G-C-T-G-C-T-G-T-T-G-T-A-G-G-A-A-C-T-C-G-A-A-C-C-A-C-C-T-T-T-C-C-A-C-A-G-A) (9CI) (CA INDEX NAME)

STN Columbus

NTE singlestranded

SEQ 1 ctggctgctg ttgtaggaac tcgaaccacc ttccacaga

L61 ANSWER 6 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:453375 CAPLUS

DN 113:53375

TI Secondary structure of 7SK and 7-2 small RNAs. Possible origin of some 7SK pseudogenes from cDNA formed through self-priming by 7SK RNA

AU Suh, Dick; Yuan, Yan; Henning, Dale; Reddy, Ram

CS Dep. Pharmacol., Baylor Coll. Med., Houston, TX, 77030, USA

SO European Journal of Biochemistry (1989), 186(1-2), 221-6

CODEN: EJBCAI; ISSN: 0014-2956

DT Journal

LA English

AB Pseudogenes having homol. to small RNAs, like 7SL, 7SK, 6S, 4.5S, U1, U2, and U3 RNAs, are abundant and dispersed in the genomes of higher eukaryotes. To better understand the possible origin of these pseudogenes, the abilities of cytoplasmic 7SL, 7SK, and nucleolar 7-2 RNAs to self-prime and result in the synthesis of cDNAs were studied. When rat 7SK RNA was used as substrate, a 294-nucleotide-long cDNA was synthesized in vitro by reverse transcriptase, indicating that the 3' end of 7SK RNA can act in a self-priming manner to generate 7SK cDNA. When 7-2 RNA was used as a substrate, a cDNA of approx. 235 nucleotides was obsd.; 7SL RNA did not act as a self-primer. Earlier studies have shown that DNAs homologous to 7SK RNA are represented by a moderately reiterated family in the mammalian genomes and many of these sequences were found to be truncated 7SK pseudogenes. In this study, one 7SK clone from the rat genome was characterized by sequencing. This clone contained 243 base pairs homologous to the 5' end of 7SK RNA, and was flanked by direct repeats. These data suggest that, as previously proposed for some U3 pseudogenes, one mechanism for the generation of truncated 7SK pseudogenes may be the integration of self-primed reverse transcripts of 7SK RNA at random genomic sites.

IT 128283-72-7, Deoxyribonucleic acid (rat Nouikoff cell clone 7SK-1 7-3 RNA pseudogene)

RL: PRP (Properties); BIOE (Biological study)
(nucleotide sequence of)

RN 128283-72-7 CAPLUS

CH DNA (rat Nouikoff cell clone 7SK-1 7-3 RNA pseudogene) (9CI) (CA INDEX NAME)

SEQ 1 gactttcaat caacaaatgg ggatgtgagg gcgatctggc tgcgacatct
51 gtcaccccat tgaatgccac gggtgattcg gctgatctcg ctggctaggc
101 gggtgtcccc tccacccctc accgtccat gtgcgtccct cccgaagctg
151 cgcgctcggg cgaagaggac gaccttcccc gaatagagga ggacgggtct
201 tcggtaagg gtatacgagt agctgcgtc ccctgctaga acctccaaac
251 agctctcaa ggtcaatcaa caaatggcca tcaacaaaac aaattcaatg
301 g

L61 ANSWER 7 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:437392 CAPLUS

STN Columbus

DN 113:37392
 TI Sex determination in ruminants using Y-chromosome-specific polynucleotides and isolation and sequencing of Y-chromosomal DNA repeat
 IN Reed, Kenneth Clifford; Lord, Eric Arthur; Matthaei, Klaus Ingo; Mann, David Andrew; Beaton, Sandra; Herr, Charles Marvin; Matthews, Margaret Ellen
 PA Advanced Riverina Holdings Ltd., Australia
 SC PCT Int. Appl., 120 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN. CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 8907154	A1	19890810	WO 1989-AU29	19890127 <--
	W: AU, JP, US				
	RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
	AU 8930451	A1	19890825	AU 1989-30451	19890127 <--
	AU 628800	B2	19920924		
	EP 397753	A1	19901122	EP 1989-902001	19890127
	EP 397753	B1	19960612		
	R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
	JP 03503358	T2	19910801	JP 1989-501848	19890127
	AT 139265	E	19960615	AT 1989-902001	19890127
	US 5459038	A	19951017	US 1993-175679	19931230
PRAI	AU 1988-6476	A	19880129		
	WO 1989-AU29	A	19890127		
	US 1990-548903	B1	19900927		
	US 1993-3695	B1	19930113		

Nucleic acids capable of hybridizing only to Y-chromosome-specific DNA sequences of ruminants are isolated and their sequences disclosed. A method of detg. sex of ruminants using polymerase chain reaction (PCR) method is also given. Thus, Y-chromosomal DNA repeats OY1.1 (3142 bp), OY4.1 (2552 bp), OY4.2 (1076 bp), OY9.2-9.5 (8010 bp), OY 11.1 (3983 bp), BRY4a (4189 bp), and BRY4c (4201 bp) of sheep; GRY.1a(a) (384 bp) and GRY.1b(a) (448 bp), as well as GRY1a and GRY1b (2589 bp) of goats; and BRY.1(a) (545 bp) and BRY.4c(i) (484 bp) of cattle were isolated from the resp. ruminant liver cell genomic library using radioactive, Y-chromosome-specific probe DNA such as BRY1 or OV11.1. The ruminant DNA repeats were subsequently detd. Genetic sexing of bovine embryos using PCR was exemplified wherein the presence of a 130-bp PCR product upon gel-electrophoresis was used as male criteria.

IT 128151-31-5. Deoxyribonucleic acid (goat clone λ -CGY1

male-specific GRY.1a(a) element)

PL: PRP (Properties)

(nucleotide sequence of)

RN 128151-31-5 CAPLUS

CN DNA (goat clone λ -CGY1 male-specific GRY.1a(a) element) (9CI) (CA

INDEX NAME)

ME dsdoublestranded

SEQ 1 acaactcaca gatttgacag actgcgagggc cctgggagtg tgacactttc
 51 tatgtgacac tgcagctgga agggagtagg aaactggcgg aggcagtgtc
 101 ggcaggtggt gtggtttttc cagctgtcac ctctctgcct ctcaagttcc
 151 aaatggcgct tcatgtgatt cataaacttg acatttttta gaactttcaa
 201 gcagctgagg catttaaacg ctgtgtgggt cttcggttct ggctgcccaa
 251 ctctcataag ctctccatag tagaagtcac gaagtacaca atcagatttc
 301 cttctgtggg atcaacaatc ttgtttggac ttgctaaact tggaaaatca
 351 gtttttgtca gtccattttc ccttaaaggt ctca

STN Columbus

L61 ANSWER 8 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:435802 CAPLUS

DN 113:35802

TI Synthesis of a gene for the protein kinase domain of the epidermal growth factor receptor and its expression in Escherichia coli

AU Farrow, Stuart N.; Kamiya, Hiroyuki; Miura, Kazunobu; Ohtsuka, Eiko; Nishimura, Susumu

CS Biol. Div., Natl. Cancer Cent. Res. Inst., Tokyo, Japan

SO European Journal of Biochemistry (1989), 184(2), 361-5

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CODEN: EJBCAI; ISSN: 0014-2956

DT Journal

LA English

AB A gene encoding the protein kinase domain of the epidermal growth factor receptor was chem. synthesized, cloned, and expressed in E. coli. The 942-base-pair gene was constructed by enzymic ligation of 56 oligonucleotides and cloned into an expression vector downstream of the E. coli trp promoter. Prodn. of active gene product was confirmed by means of a protein kinase assay, demonstrating that the enzymic activity of the protein kinase domain of the epidermal growth factor receptor is retained after expression in E. coli.

IT 124203-25-6P

RI: RCT (Reactant); PREP (Preparation); RACT (Reactant or reagent) (prepn. and nucleotide coupling reactions of)

BN 124203-25-6 CAPLUS

CN GGAAGGAGGCAAGTTCAGGCAAGGATGAGGCTGCGCAATGATGTTATCTT
(CA INDEX NAME)

AB 124203-25-6P

BT 124203-25-6P
GGAAGGAGGCAAGTTCAGGCAAGGATGAGGCTGCGCAATGATGTTATCTT

L61 ANSWER 9 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:435803 CAPLUS

DN 113:35803

TI Molecular cloning of metallothionein cDNA and analysis of metallothionein gene expression in winter flounder tissues

AU Chan, King Ming; Davidson, William S.; Hew, Choy L.; Fletcher, Garth L.

CS Acad. Sci. Cent., Mem. Univ. Newfoundland, St. John's, NF, A1C 5S7, Can.

SO Canadian Journal of Zoology (1989), 67(10), 2520-7

CODEN: CJZCAG; ISSN: 0008-4301

DT Journal

LA English

AB Investigations into the precise role played by metallothionein (MT) in heavy-metal metab. have been hampered by difficulties in pos. identifying and quantifying MT in fish tissues. This study describes the development of an antisense MT RNA (crRNA) probe that will enable MT mRNA levels to be measured with a high degree of specificity and precision. Cadmium chloride administration induces the prodn. of MT mRNA in the liver and kidney of winter flounder (Pseudopleuronectes americanus). Poly(A)+ RNA purified from liver samples of winter flounder after cadmium chloride injections was used to construct a cDNA library. Several recombinant clones made complementary to MT mRNA were selected from this cDNA library by an oligonucleotide derived from the N-terminal amino acid sequence of winter flounder metallothionein. Sequence anal. of 2 of the cDNA inserts

STN Columbus

gave the structure of the entire 3' untranslated region, a coding region corresponding to winter flounder MT, and 49 nucleotides of the 5' untranslated region. One of the flounder MT cDNAs, pWFMTc4, was subcloned into a RNA probe plasmid and transcribed to produce antisense MT RNA (cRNA). The MT cRNA was then used to detect the induction of MT mRNA prodn. in the liver of winter flounder, following the administration of Cu2+, Zn2+, Cd2+, Pb2+ and Hg2+. The time required for the induction of hepatic MT mRNA by a single injection of Cd2+ was approx. 96 h. Dexamethasone did not induce an increase of MT mRNA in any of the winter flounder tissues examd. (liver, kidney, heart, brain, intestinal scrape, and gill filament), whereas Cd2+ induced MT mRNA in all of the tissues except brain, where the constitutive level of expression was high.

IT 127385-13-1, Deoxyribonucleic acid (Pseudopleuronectes americanus clone pWFMTc69 metallothionein messenger RNA-complementary)
 RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)
 RN 127385-13-1 CAPLUS
 CN DNA (Pseudopleuronectes americanus clone pWFMTc69 metallothionein cDNA) (9CI) (CA INDEX NAME)
 NFE doublestranded

SEQ 1 atggatccct gccaatgctc caagactgga acctgcaact gcggaggatc
 51 ttgcacctgc aagaactgca gctgcaccac ctgcaacaag agctgctgcc
 101 catgctgccc atccggctgc cccaagtgcg cctctggctg cgtgtgcaaa
 151 gggaagacat gcgacaccac ttgctgtcag tga

661 ANSWER 10 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

EXPI-1989

AN 1989-01-1555 CAPLUS

DN 112-1111-55

TI Nucleotide sequences from the colicin E5, E6 and E9 operons: presence of a degenerate transposon-like structure in the ColE9-J plasmid.

AU Lau, Peter C. K.; Condie, Janet A.

CS Biotechnol. Res. Inst., Natl. Res. Council, Canada, Montreal, QC, H4P 2R2, Can.

SO Molecular and General Genetics (1989), 217(2-3), 269-77

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CODEN: MGGEAE; ISSN: 0026-8925

DT Journal

LA English

AB The nucleotide sequences of 1288 bp of plasmid ColE5-099, 1509 bp of ColE6-CT14, and 2099 bp of ColE9-J were detd. These sequences encompass the structural gene for the C-terminal receptor-binding and nuclease domains of colicins E5, and E6, and E9, their cis- or trans-acting immunity proteins and four lysis proteins, including an atypical one of non-lipoprotein nature (Lys*) present in the ColE9-J plasmid. The ColE6 gene organization, in the order coli-imm-E8imm-lys, is identical to that found in the double-immunity gene system of ColE3-CA38 (an RNase producer). The corresponding genes in the two plasmids are 87%-94% homologous. In ColE9-J, the genes are organized as coli-imm-lys*-E5imm-lys. The E9 coli-imm gene pair is homologous to the colicin E2-P9 type (a DNase producer). Downstream from E9imm is an E5imm (designated E5imm[E9]) which is trans-acting. Neither the predicted structures of E5imm[E9] nor the cis-acting Imm resident in the ColE5-099 plasmid which differs by a single amino acid shows any resemblance to other immunity structures which have been sequenced. Furthermore, the E5cl sequences differ from those previously for other colicins except for the conserved btuB-specified receptor-binding domain. A novel 205 nucleotide long insertion sequence

STN Columbus

is found in the ColE9-J plasmid. This insertion sequence, which was named ISE9, has featured reminiscent of the degenerate transposon IS101 found in plasmid pSC101. One effect of ISE9 is the presence of the atypical lysis gene, *lys**. The presence of a transposon-like element in the ColE9 plasmid exemplifies a new phenomenon relevant to the evolution of colicin E plasmids.

IT 126547-55-5, Deoxyribonucleic acid (plasmid ColE6-CT14 gene *lys*)

RL: PRP (Properties); BIOL (Biological study)

(nucleotide sequence of)

RN 126547-55-5 CAPLUS

CN DNA (plasmid ColE6-CT14 clone pAM362 gene *lys*) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaaaaaaa taacagggat tattttattg cttcttgag tcattattct
51 ggctgcatgt caggcaact atatcgtga tggtcagggc gggactgtat
101 caccgtcgtc aactgctgaa ctgaccggag tggaaacgca gtaa

L61. ANSWER 11 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:193120 CAPLUS

DN 112:193120

TI Production and engineering of human lysozyme using recombinant DNA techniques

AU Muraki, Michiro; Jigami, Yoshifumi; Tanaka, Hideaki

CS Natl. Chem. Lab. Ind., Tsukuba, Japan

SO Kagaku Gijutsu Kenkyusho Hokoku (1989), 84(8), 495-501

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CODEN: KKKHEP; ISSN: 0388-3213

DT Journal

LA Japanese

AB An artificial gene encoding human lysozyme was chem. synthesized and expressed both in *Escherichia coli* and *Saccharomyces cerevisiae*. The product in *E. coli* formed insol. aggregates and had no enzymic activity. Urea treatment of the aggregates regenerated the enzymic activity partly, but the yield was very low. To examine the extracellular prodn. of human lysozyme by *S. cerevisiae*, the signal peptide gene of chicken lysozyme was fused to the 5'-end of the mature human lysozyme gene. The *S. cerevisiae* cells harboring the chimeric prelysozyme gene secreted the enzymically active human lysozyme into the culture medium. A single chromatog. with a cation exchanger gave an almost pure enzyme with an identical specific activity to that of the authentic human lysozyme. The identity of the N-terminal amino acid sequence of the purified enzyme compared with that of authentic human lysozyme indicated correct processing of the chicken signal peptide and the successful prodn. of human lysozyme occurred in *S. cerevisiae* cells. Amino acid residues composing the catalytic cleft of human lysozyme were changed by site-specific mutagenesis. Conversions of catalytic residues, Glu-35 to Asp and/or Asp-53 to Glu, remarkably decreased the enzymic activity, reflecting the fragility of the catalytic site. Mutagenesis of the three arom. residues which are conserved among the same type lysozymes revealed that an arom. residue at position 63 and a tryptophan at 64 were crucial for the recognition of substrates. On the other hand, a tryptophan at 109 was essential for the efficient cleavage of the substrate, but not for the substrate recognition. Modification of the charge state of the residue at 115 changed the cleavage pattern of an oligosaccharide substrate, N-acetylglucosamine pentamer, suggesting the possibility of the artificial alteration of products in the enzymic reaction. The effect of the change in surface charge of the enzyme was also examd. The mutant human lysozymes with an increased or a decreased

STN Columbus

pos. charge showed higher lytic activity than the wild-type enzyme under conditions not optimal for the wild-type enzyme in regard to the ionic strength and pH. These results demonstrate the effectiveness of a protein engineering approach in improving the protein function as well as in elucidating the structure-function relationships of proteins.

IT 126627-25-6P, Deoxyribonucleic acid (chicken prelysozyme signal peptide-specifying)

RL: PREP (Preparation)

(prepn. of, for lysozyme synthetic gene cloning)

RN 126627-25-6 CAPLUS

CN DNA (chicken prelysozyme signal peptide-specifying) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 tcgactcgat gaggtctttg ctaatcttgg tgctttgctt cctgccctg
51 gctgctctgg ggaaggtttt

1 cgaaacacatt cccagagca gccaggggca ggaagcaaag caccaagatt
51 agcaaagacc tcatcgag

L61 ANSWER 12 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:173112 CAPLUS

DN 1121173112

TI Molecular structure and immunity specificity of colicin E6, an evolutionary intermediate between E-group colicins and cloacin DF13

AU Akutsu, Akiko; Masaki, Haruhiko; Ohta, Takahisa

OS Dep. Agric. Chem., Univ. Tokyo, Tokyo, 113, Japan

SO Journal of Bacteriology (1989), 171(12), 6430-6

====

CODEN JBAAY; ISSN: 0021-9193

DT JOURNAL

LA English

The primary structure of a 3.1-kilobase E6 or E3 segment carrying colicin and related genes was determined. Plasmid ColE6-CT14 showed striking homology to ColE6-CA38 throughout this segment, including homology to the secondary immunity gene, immE8, downstream of the E6 or E3 immunity gene. The ColE6-CA38 and ColE6-CT14 sequences, however, contained an exceptional hot spot region encoding both the colicin-active domain (RNase region) and the immunity protein, reflecting their different immunity specificities. On the other hand, some chimeric plasmids were constructed through homologous recombination between colicin E3 and cloacin DF13 operons. The resulting plasmids were deduced to produce chimeric colicins with a colicin E3-type N-terminal part, a cloacin DF13-type C-terminal-active domain, and the DF13 immunity protein. The killing spectra of the chimeric colicins and the immunities of the plasmids were identical to those of colicin E6 and ColE6-CT14, respectively, showing that the colicin E6 immunity specificity is completely equivalent to that of cloacin DF13. Nevertheless, colicin E6 has been found to show a sequence diversity from cloacin DF13 almost to the same extent as that from colicin E3 in their RNase and immunity regions, indicating that only a small number of amino acids defines the immunity specificity for discrimination between colicins E3 and E6 (or cloacin DF13).

IT 126627-25-5, Deoxyribonucleic acid (plasmid ColE6-CT14 clone pAM362 gene lys)

RL: PREP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 126627-25-5 CAPLUS

CN DNA (plasmid ColE6-CT14 clone pAM362 gene lys) (9CI) (CA INDEX NAME)

STN Columbus

NTE doublestranded

SEQ 1 atgaaaaaaa taacagggat tattttattg cttcttcag tcattattct
51 ggctgcatgt caggcaact atatccgtga tggtcagggc gggactgtat
101 caccgtcgtc aactgctgaa ctgaccggag tggaaacgca gtaa

L61 ANSWER 13 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:152605 CAPLUS

DN 112:152605

TI Multiple copies of the coding regions for the light-harvesting B800-850 α - and β -polypeptides are present in the *Rhodopseudomonas palustris* genome

AU Tadros, Monier Habib; Waterkamp, Karin

CS Inst. Biol., Freiburg, D-7800, Fed. Rep. Ger.

SO EMBO Journal (1989), 8(5), 1303-8

====

CODEN: EMJODG; ISSN: 0261-4189

DT Journal

LA English

AB A reverse-phase HPLC System for isolation of the water insol. α - and β -polypeptides of the light-harvesting complex II (LH II) of *R. palustris* without employment of any detergent was developed. The material obtained was of high purity and suitable for direct microsequence anal. Chromatog. anal. could resolve ≥ 2 major β -polypeptides, $\beta\alpha$ and $\beta\beta$, 2 major α -polypeptides, $\alpha\alpha$ and $\alpha\beta$, and 2 addnl. minor polypeptides. N-terminal acid sequencing shows that the resolved peaks correspond to different polypeptide species, and that the minor species have an N-terminal sequence identical to that of the $\alpha\beta$ polypeptide. An oligonucleotide derived from the N-terminal sequence of the $\alpha\beta$ polypeptide was utilized to screen a genomic library from *R. palustris*. Several independent clones were characterized by Southern blot and nucleotide sequence anal. *R. palustris* contains 24 different clusters of β and α genes. Two clones contain sequences potentially coding for $\beta\alpha$ - $\alpha\alpha$ and $\beta\beta$ - $\alpha\beta$ polypeptides; and 2 addnl. clones potentially coding for β and α peptides which were named $\beta\gamma$ - $\alpha\gamma$ and $\beta\delta$ - $\alpha\delta$, which did not correspond to the major purified polypeptides. In addn. to the protein chem. data, the conservation at the amino acid level and the presence of canonical ribosomal binding sites upstream of each of the identified genes strongly suggest that all 4 coding regions are expressed.

IT 125858-45-6, Deoxyribonucleic acid (*Rhodopseudomonas palustris* clone .vphi.-4 light-harvesting protein B 800-850 β isoform a gene)
125858-47-1, Deoxyribonucleic acid (*Rhodopseudomonas palustris* clone .vphi.-5 light-harvesting protein B 800-850 β isoform b gene)
125858-51-7, Deoxyribonucleic acid (*Rhodopseudomonas palustris* clone .vphi.-1 light-harvesting protein B 800-850 β isoform d gene)
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 125858-45-9 CAPLUS

CN DNA (*Rhodopseudomonas palustris* clone .vphi.-4 light-harvesting protein B 800-850 β isoform a gene) (9CT) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggctgaca agacgtgac cggcctgac gtcgaggagt ccgaagagct
51 ccacaagcac gtgatcgatg gcaccgcat ttcggtgcg atcgcgatcg

STN Columbus

101 tcgcgcactt cctcgcctac gtttactcgc cctggctgca ctaa

RN 125858-47-1 CAPLUS

CN DNA (Rhodospseudomonas palustris clone .vphi.-6 light-harvesting protein B
 800-850B isoform b gene) (9CI) (CA INDEX NAME)

NTE doublestranded

```

SE2      1 atggcagacg atccgaacaa ggtctggccg accggtctga cgatcgcgga
        51 atcggaaagag ctccacaagc atgtgatcga cggcacgcgc attttcggcg
       101 cgatcgccat cgtcgctcac ttctggcgt atgtttattc gccctggctg
       151 cactaa

```

RN 125858-51-7 CAPLUS

RN 125858-517 CA INDEX
 CN DNA (Rhodospseudomonas palustris clone .vphi.-1 light-harvesting protein B
 800-850β isoform d gene) (9CI) (CA INDEX NAME)

NTE doublestranded

```
SEQ      1 atcgtagacg atccgaacaa ggtctggcgg actgggctga ccatcgcgga
      51 atcgggaagag ctccacaagc acgtgatcga tggttcgcgg attttcgtgg
     101 ccacgcgcgat cgtggcgcgt ttctctggcg acgtttactc gccctggctg
     151 cactaa
```

LS1 CHANGE 24 OF 52 CAPLUS. COPYRIGHT 2005 ACS on STN

[Full Text](#)

AN 1990:103420 CAPLUS

DN 112:135439

TI Isolation and structural characterization of cDNA clones encoding the mating pheromone Er-1 secreted by the ciliate-Euplotes raikovi

AU Miceli, Cristina; La Terza, Antonietta; Melli, Marialuisa

CS Dep. Cell Biol., Univ. Camerino, Camerino, 62032, Italy

SO Proceedings of the National Academy of Sciences of the United States of America (1989), 86(9), 3016-20

CODEN: PNASA6; ISSN: 0027-8424.

DT Journa

LA English

AB CDNA clones comprising the entire coding region for the mating pheromone Er-1 of *E. raikovi* were isolated by oligonucleotide screening of two cDNA libraries in the vectors λ gt10 and pUC12. The cDNA sequence contains an open reading frame of 75 amino acids that constitute pre-pro-Er-1. The amino acid sequence of secreted Er-1 starts at aspartic acid-38 of pre-pro-Er-1 and completely matches that known by direct Er-1 protein sequencing. The coding region of Er-1 cDNA ends with codon TAA, which specifies glutamine in other ciliates. The 5'- and 3'-noncoding regions contain, resp., two and one inverted repeats. The 3'-noncoding-region inverted repeat, which includes the unusual polyadenylation signal AACAAA, has been related to RNA 3'-terminus formation.

IP 125546-74-9; Deoxyribonucleic acid (Euplotes raikovi clone
λ4/p3/5b euplomone r 1 messenger RNA-complementary)

PL: PRP: (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 125546-74-9 CAPLUS

STN Columbus

CN DNA (Euplotes raikovi clone λ 4/p3/5b euplomone r 1 cDNA) (9CI) (CA INDEX NAME)

NTE dcublestranded

SEQ 1 atgaacaaac tagcaattct cgctatcatc gctatggtag tcttcagcgc
51 caacgccttc agattccaaa gcagattgag atcaaatgta gaagctaaga
101 caggagatgc ttgtgagcaa gctgcaatcc agtgtgttga gtcagcatgt
151 gaaagtcttt gtacagaagg tgaagataga actggctgct atatgtacat
201 ctattctaac tgcccacctt atgtctaa

L61 ANSWER 15 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:133303 CAPLUS

DN 112:133303

TI Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular cloning, sequence, and expression in Escherichia coli

AU Duchene, Michael; Barron, Carlos; Schweizer, Andrea; Von Specht, Bernd Ulrich; Domdey, Horst

CS Lab. Mol. Biol., Ludwig-Maximilians-Univ. Muenchen, Martinsried, D-8033, Fed. Rep. Ger.

SC Journal of Bacteriology (1989), 171(8), 4130-7

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CODEN: JOBAAY; ISSN: 0021-9193

DT Journal

LA English

AB Lipoprotein I (OprI) is one of the major proteins of the outer membrane of Pseudomonas aeruginosa. Like porin protein F (OprF), it is a vaccine candidate because it antigenically cross reacts with all serotype strains of the International Antigenic Typing Scheme. Since lipoprotein I was expressed in Escherichia coli under the control of its own promoter, it was possible to isolate the gene by screening a (λ) EMBL3 phage library with a mouse monoclonal antibody directed against lipoprotein I. The monocistronic OprI mRNA encodes a precursor protein of 93 amino acid residues, including a signal peptide of 19 residues. The mature protein has a mol.wt. of 6950, not including bound glycerol and lipid. Although the amino acid sequences of protein I of P. aeruginosa and Braun's lipoprotein of E. coli differ considerably (only 30.1% identical amino acid residues), the sequences at the signal peptidase cleavage site and at the C-terminus, which is the attachment site to peptidoglycan in E. coli, are identical. Using lipoprotein I expressed in E. coli, it can now be tested whether this protein alone, without P. aeruginosa lipopolysaccharide contaminations, has a protective effect against P. aeruginosa infections.

IT 125723-82-2; Deoxyribonucleic acid (Pseudomonas aeruginosa clone pITaq1 lipoprotein I gene)

EN: PEP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 125723-82-2 CAPLUS

CN LNA (Pseudomonas aeruginosa clone pITaq1 lipoprotein I gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaacaaac tcttgaaatt ctctgctctg gctctggctg ctgttctggc
51 caccggttgc agcagccact ccaaagaaac cgaagctcgt ctgaccgcta
101 ccgaagacgc agctgctcgt gctcaggctc gcgctgacga agcctatcgc
151 aaggtctgac agctcttggg cgctgctcag aaagctcagc agaccgctga
201 cgaggctaac gagcgtgccc tgccgatgct ggaaaaagcc agccgcaagt

STN Columbus

251 aa

L61 ANSWER 16 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:71242 CAPLUS

DN 112:71242

TI Nucleotide sequences of *Caenorhabditis elegans* core histone genes. Genes for different histone classes share common flanking sequence elements

AU Roberts, Susan Boseman; Emmons, Scott W.; Childs, Geoffrey

CS Dep. Genet., Albert Einstein Coll. Med., Bronx, NY, 10461, USA

SO Journal of Molecular Biology (1989), 206(4), 567-77

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CODEN: JMOBAK; ISSN: 0022-2835

DT Journal

LA English

AB The nucleotide sequence of core histone genes and flanking regions from 2 of approx. 11 different genomic histone clusters of the nematode *C. elegans* were detd. Four histone genes from one cluster (H3, H4, H2B, H2A) and 2 histone genes from another (H4 and H2A) were analyzed. The predicted amino acid sequences of the two H4 and H2A proteins from the 2 clusters are identical, whereas the nucleotide sequences of the genes have diverged 9% (H2A) and 12% (H4). Flanking sequences, which are mostly not similar, were compared to identify putative regulatory elements. A conserved sequence of 34 base pairs is present 19 to 42 nucleotides 3' of the termination codon of all the genes. Within the conserved sequence is a 16-base dyad sequence homologous to the one typically found at the 3' end of histone genes from higher eukaryotes. The *C. elegans* core histone genes are organized as divergently transcribed pairs of H3-H4 and H2A-H2B and contain 5' conserved sequence elements in the shared spacer regions. One of the sequence elements, 5'-CTCCNCCTNCCCACCNCANA-3', is located immediately upstream from the canonical TATA homol. of each gene. Another sequence element, 5'-CTGCGGGGACACATNT-3', is present in the spacer of each geneotypic pair. These two 5' conserved sequences are not present in the promoter region of histone genes from other organisms, where 5' conserved sequences are usually different for each histone class. They are also not found in non-histone genes of *C. elegans*. These putative regulatory sequences of *C. elegans* core histone genes are similar to the regulatory elements of both higher and lower eukaryotes. The coding regions of the genes and the 3' regulatory sequences are similar to those of higher eukaryotes, whereas the presence of common 5' sequence elements upstream from genes of different histone classes is similar to histone promoter elements in yeast.

PT 125122-13-6, Deoxyribonucleic acid (*Caenorhabditis elegans* clone

pCeh-1 gene his-3)

AD PRP (Properties): BICL (Biological study)

(nucleotide sequence of)

RN 125122-13-6 CAPLUS

CH DNA (*Caenorhabditis elegans* clone pCeh-1 gene his-3) (9CI) (CA INDEX NAME)

FE Doublestranded

```

SEQ      1 atgtctggac gcggaaggg aggcgaagcc aagaccggag gaaaggccaa
        51 gtcccgctca tcaagagccg gactccaatt cccagttggt cgtcttcacc
       101 gtattctccg taaaggaaac tacgtcaaac gtgttgaggc cggagcccca
       151 gtttacctgg ctgccgttct tgagtacctc gctgctgagg ttctcgagtt
       201 ggctggaaac gctgcccggtg ataacaagaa gaccagaatt gccccaagac
       251 atctccaact ggccgtccgt aacgatgagg agttgaacaa actgttggtt
       301 ggagtaacca tcgccaaggg aggagttctt ccaaatatcc aagctgttct

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STN Columbus

351 tttgccgaag aaaaccggag gagacaagga atag

AL61 ANSWER 17 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:17045 CAPLUS

DN 112:17045

TI Structure and evolution of somatostatin genes

AU Su, Chung Jey; White, James W.; Li, Wen Hsiung; Luo, Chi Cheng; Frazier, Marsha L.; Saunders, Grady F.; Chan, Lawrence

CS Syst. Cancer Cent., Univ. Texas, Houston, TX, 77030, USA

SO Molecular Endocrinology (1988), 2(3), 209-16

====

CODEN: MOENEN; ISSN: 0888-8809

DT Journal

LA English

AB A bovine pancreatic preprosomatostatin cDNA clone was isolated and sequenced. Although it encodes a predicted 116-amino acid preprosomatostatin that is very similar in primary structure to those deduced from other mammalian preprosomatostatin cDNAs, there are some differences in amino acid compn. Hybridization of this clone to Northern blots of fetal bovine pancreatic poly(A)+ RNA reveals a mRNA of 700 nucleotides. Evlution of the preprosomatostatin genes was studied by statistical anal. of anglerfish, catfish, bovine, rat, and human cDNA sequences. The results suggest that the 2 somatostatin genes present in both anglerfish and catfish were the result of a gene duplication event in a common ancestor of anglerfish and catfish.

IT 124383-94-2, Deoxyribonucleic acid (ox clone FBPS-2 somatostatin messenger RNA-complementary)

RL EXP (Properties); BIOL (Biological study)
(nucleotide sequence of)

EN 124383-94-2 CAPLUS

CN DNA (cattle clone FBPS-2 somatostatin cDNA) (9CI) (CA INDEX NAME)

NFE doublestranded

SEQ 1...ttgtgtgctt gcgcctcca gtgcgcgtg gccgcgtct ccatcgtcct
51...ggctcttggc ggtgtcaccg gcgcgcctc ggtccccgg ctccgtcagt
101...ttctgcagaa atccctggct gctgdcgctg gcaagcagga actggccaag
151...tactcttgg cagagctgct gtctgaacc aaccagacag agattgatgc
201...cctggagcct gaaatattgt ccagagctgc tgagcaggat gaaatgaggc
251...tggagctgca gagatctgct aactcaaacc cggccatggc accccgagaa
301...cgcaaaagctg gctgcagaa tttcttctgg aagactttca catcctgtta
351...a

AL61 ANSWER 18 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1989:547785 CAPLUS

DN 111:147785

TI Nucleotide sequence of cDNA for rat liver and brain cytochrome c oxidase subunit VIa (Vb)

AU Goto, Yoshitaka; Amuro, Nacki; Okazaki, Taro

CS Dep. Biochem., Nippon Med. Sch., Tokyo, 113, Japan

SO Nucleic Acids Research (1989), 17(15), 6388

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CODEN: NARHAD; ISSN: 0305-1048

DT Journal

STN Columbus

LA English

AB The nucleotide sequence of the cDNA for cytochrome c oxidase [EC 1.9.3.1] subunit VIa (Vb) from rat liver is reported. The cDNA insert of the liver was 434 bp, contg. a 5'-untranslated region of 54 bp, a coding region of 297 bp, a 3'-untranslated region of 83 bp and a poly(A) tail. The deduced amino acid sequence is composed of 99 residues, including the amino terminal methionine, and differs from the amino acid sequence of bovine heart mature subunit VIa by 17 out of 98 residues. Since the nucleotide sequence of rat brain cDNA was found to be completely identical with that of liver, it is assumed that the same gene is expressed in both the liver and brain of rat.

IT 123008-93-5, Deoxyribonucleic acid (rat liver cytochrome oxidase subunit VIa messenger RNA-complementary)

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 123008-93-5 CAPLUS

CN DNA (rat liver cytochrome oxidase subunit VIa cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggcctctg gaggtggtgt ccctactgat gaggagcagg ctaccgggct
51 ggagagggag atcatgatag cagcacagag gggactggat ccatacaata
101 tgctacctcc aaaggcagct tcgggcacca aggaagaccc caatctagtc
151 ccattccgta gcaacaagag aatagtgggc tgcattctgtg aagaggacaa
201 ctgcactgtc atctggttct ggctgcacca aggcgagagc cagcgatgcc
251 ccaactgtgg aacacattac aagttggtgc cctaccaaatt ggtccactga

LS17 NUMBER 19 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994-502169 CAPLUS

DT 11/1/1994

AB A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes.

AN Brown, Keith D.; Zurawski, Sandra M.; Mosmann, Timothy R.; Zurawski, Gerard

CS Res. Inst. Mol. Cell. Biol., DNAX, Palo Alto, CA, 94304, USA

SO Journal of Immunology (1989), 142(2), 679-87

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CODEN: JOIMA3; ISSN: 0022-1767

DT Journal

LA English

AB Four cDNA clones that encode mRNA expressed more abundantly in Con A-activated mouse helper T cells than by resting T cells were isolated and characterized. One mRNA encoded a ~14-kDa protein with a hydrophobic N-terminal sequence and was abundantly expressed by the Th 2 subset of T-helper (Th) cells, but was not expressed by Th 1 cells. The remaining 3 mRNA encoded related ~8-kDa secreted proteins that are part of a family of small, secreted, and inducible mouse and human proteins. This family of proteins is itself distantly related to another family of growth and inflammatory factors that are assocd. with various lymphoid and fibroblast activation phenomena. One of the small, inducible, secreted proteins has a predicted mature N terminus identical to that of the previously described macrophage inflammatory protein.

IT 123009-54-4, Deoxyribonucleic acid (mouse clone P500 protein SIS

c-messenger RNA-complementary)

RL: PRP (Properties)

(nucleotide sequence of)

STN Columbus

RN 122783-54-4 CAPLUS
CN DNA (mouse clone P500 protein SIS ϵ -isoform cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaaaccca ctgccatggc actgatgtgc ctgctgctgg ctgccgtgtg
51 gatacaggat gttgacagca agagcatgct tacggtctcc aatagctgct
101 gcttgaacac cttgaagaaa gagcttcccc tgaagtttat ccagtgttac
151 agaaagatgg gctcctcctg tcctgatccc ccagctgtgg tagtcaggag
201 ttcaggggtc cctgggtctca cagaagcaga gaagactgtt acagattcca
251 gtgagtga

L61 ANSWER 20 OF 62 CAPLUS COPYRIGHT 2005 ACS.cn STN

Full Text

AN 1989:491439 CAPLUS

DN 111:91439

TI Cloning and sequence analysis of cDNA encoding a precursor for porcine brain natriuretic peptide

AU Maekawa, Keiji; Sudo, Tetsuji; Furusawa, Mitsuru; Minamino, Naoto; Kangawa, Kenji; Okubo, Hiroaki; Nakanishi, Shigetaba; Matsuo, Hisayuki

CS Daiichi Seiyaku Co. Ltd., Tokyo, 134, Japan

SO Biochemical and Biophysical Research Communications (1983), 157(1), 410-16

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CODEN ABRC9; ISSN: 0006-291X

LT Journal

LA English

AB Brain natriuretic peptide (BNP) is a new type of natriuretic peptide recently identified in porcine brain. Since the highest concn. of BNP was found in the cardiac atrium, the cDNA library of porcine cardiac atrium was constructed, and the cDNA encoding a BNP precursor was isolated and sequenced. The precursor for porcine BNP (porcine prepro-BNP) is 131 amino acids in length, including a 25 residue putative signal peptide at the N-terminus. Porcine BNP structure is located at the C-terminus of the precursor and is directly followed by a termination codon. Based on structural data recently obtained for γ -BNP (a main storage form of BNP in the heart), prepro-BNP is processed to 106-residue γ -BNP by removal of the signal peptide in the heart, and to low mol. wt. forms, such as BNP-26 and BNP-32, in the brain.

IT 122006-95-5, Deoxyribonucleic acid (pig brain natriuretic factor messenger RNA-complementary) 122006-96-6, Deoxyribonucleic acid (pig clone pBNP34 brain natriuretic factor messenger RNA-complementary)

SC: PEP (Properties); BIO: (Biological study)
(nucleotide sequence of)

FN 122006-95-5. CAPLUS

CN DNA (porcine brain natriuretic peptide cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgggcccc ggatggcgct tccccgcgtg ctctgctcc tgttcttgca
51 cctgttgcgt ctaggatgcc gttcccatcc actgggtggc gctggcctgg
101 cctcagaact gccagggata caggagctgc tggaccgcct gcgagacagg
151 gtctccgagc tgcaggcgga gccgacggac ctggagcccc tccggcagga
201 ccgtggcctc acagaagcct gggaggcgag ggaagcagc cccacggggg
251 ttcttgggac cgcagtagc atcttccaag tcctccgggg aatacgagc
301 cccaagacga tgcgtgactc tggctgcttt gggcgaggc tggaccggat
351 cggctccctc agcggcctgg gctgcaatgt gctcaggagg tactga

STN Columbus

RN 122006-96-6 CAPLUS
 CN DNA (swine clone pBNP84 brain natriuretic peptide cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgggcccc ggatggcgct tccccgcgtg ctctgctcc tgttcttgca
 51 cctgttgctg ctaggatgcc gttcctatcc actgggtggc gctggcctgg
 101 cctcagaact gccagggata caggagctgc tggaccgcct gcgagacagg
 151 gtctccgagc tgcaggcgga gcggacggac ctggagcccc tccggcagga
 201 ccgtggcctc acagaagcct gggaggcgag ggaagcagcc cccacggggg
 251 ttcttggggc ccgcagtagc atcttccaag tcctccgggg aatacgcagc
 301 cccaagacga tgcgtgactc tggctgcttt gggcggaggc tggaccggat
 351 cggctccctc agcggcctgg gctgcaatgt gctcaggagg tactga

L61 ANSWER 21 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1989:451444 CAPLUS

DN 111:51444

TI Nucleotide sequence of a cDNA encoding a larval α -globin chain of the amphibian *Pleurodeles waltlii*

AU Flavin, Michelle; Valentin, Colette; Meunier-Rotival, Michele; Cohen-Solal, Michel

CS Hop. Henri Mondor, Creteil, 94010, Fr.

SO Nucleic Acids Research (1989), 17(7), 2850

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CODING NARHAD; ISSN: 0305-1048

DT English

LA English

AB In *P. waltlii*, Hb undergoes an ontogenic switch from larval to adult form. This switch is inducible by thyroid hormones and represents an alternative system to study the regulation of the sequential activation of the globin genes during erythroid differentiation. A library of erythrocyte cDNAs has been constructed from larvae of *P. waltlii* at a stage where larval and adult globin genes are expressed simultaneously. The clones corresponding to larval or adult genes were sepd. by differential screening and identified by hybridization selection and in vitro translation of the selected mRNAs. The sequence of an α -globin cDNA found only at early stages of development is reported.

IT 121630-86-2, Deoxyribonucleic acid (*Pleurodeles waltlii*, α -globin messenger RNA-complementary)

RE: PEE (Properties); BIOL (Biological study)

(nucleotide sequence of)

RN 121630-86-2 CAPLUS

CN DNA (*Pleurodeles waltlii* α -globin cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 gttctgtcag ctgaagaagg aggtgaagcc ctggacaggc tgtttgccag
 51 cttcgccag acgaggacct acttcagcca cttcgacctc tccccgggct
 101 ctgctgacgt gaaacgacat ggaggcaagg tctaagcgc catcggtgaa
 151 gcagccaagc acatcgacag catggaccag gccctgtcta aactgagcga
 201 cctgcacgac tacaacctcc gcgtggagcc cggaaatttc cagctgctgt
 251 ctactgcat tcaggctgtg ctggctgcc acttccctgc cgacttgacc
 301 cctcagtgcc aggtgctg. ggacaagttc ctggccgcag tgtctgccgt
 351 cctgacctcc aagtacagat aa.

STN Columbus

L61 ANSWER 22 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1989:451406 CAPLUS

DN 111:51406

TI A gene expressed in the endoderm of the sea urchin embryo

AU Dolecki, Gregory J.; Lum, Richard; Humphreys, Tom

CS Pacific Biomed. Res. Cent., Univ. Hawaii, Honolulu, HI, 96813, USA

SO DNA (1988), 7(9), 637-43

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CODEN: DNAADR; ISSN: 0198-0238

DT Journal

LA English

AB Using a previously cloned, developmentally regulated mRNA sequence expressed predominantly in the endoderm of sea urchin pluteus larvae, genomic clones and addnl. cDNA clones were isolated to define the gene and the protein it encodes. Nucleic acid sequencing revealed that the gene (termed 217 gene) consists of 4 exons interrupted by 3 introns and spans ~ 3600 bp. It encodes a low-mol.-wt. protein with polar ends. A stretch of Glu and Asp residues at its carboxyl terminus suggests that it is a nucleic acid-binding protein and a stretch of 4 Lys residues near the amino terminus suggests a nuclear localization signal.

IT 121605-30-5, Deoxyribonucleic acid (Tripneustes gratilla clone

λ2171 gene 217 coding region)

RE: PRP (Properties); BIOL (Biological study)

(nucleotide sequence of)

RN 121605-30-5 CAPLUS

CN DNA (Tripneustes gratilla clone λ2171 gene 217 coding region) (9CI)

(DB INDEX NAME)

NTE Unlesstranded

SEQ 1 atgcctggta aaacagctca aaaggggtgt cgcctctccg gaaagggcaa
 51 gaaagaagaag cagacactga agttcacaat cgactgcact ctgccagttg
 101 tatggcat tatggatgca cctaactttg sacagttcct ccaggaacgc
 151 gaaaggtga acggcaagac caagaacctg acaaccaaca tcgtcatcga
 201 gaaagaagaag agcaaggtca ccgttacttc tgagattgct ttctccaaaa
 251 ggtacctcaa gtatttgacc aagaagtacc tgaagaagaa caacctccgt
 301 gactggctgc gtgttggtgc tgccaacaag gaaagctacg aactccgata
 351 attccagatc aaccaggatg acgaggaaga agaggacgac taa

L61 ANSWER 23 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1989:44413 CAPLUS

DN 111:34413

TI Nucleotide sequence and transcription of a rat tRNAPhe gene and a neighboring Alu-like element

AU Rosen, Ada; Daniel, Violet

CS Dep. Biochem., Weizmann Inst. Sci., Rehovot, 76100, Israel

SO Gene (1988), 69(2), 275-85

====

CODEN: GENED6; ISSN: 0378-1119

DT Journal

LA English

AB A phage λ Ch4A clone contg. a 22-kb rat DNA insert was isolated and found to contain a solitary tRNAGAAPhe gene and, 436 bp downstream of it, an Alu-like element. The nucleotide sequence of a 1141-bp DNA fragment contg. these genes was detd. The rat tRNAGAAPhe gene, with the exception

STN Columbus

of an addnl. A in the extra arm, has a sequence identical to that of a rabbit liver tRNAPhe. The Alu-like element belongs to the rodent B2 family of short interspersed repetitive nucleotide sequences. This repetitive element, B2Phe, is flanked by 12-bp direct repeats, contains an internal split promoter (block A and block B) for RNA polymerase III and is devoid of an A-rich segment at the 3' end. Like other members of the B2 family, the B2Phe element presents 64% sequence homol. with rat serine tRNA and contains a serine (GCT) anticodon. Both tRNAGAAPhe gene and B2Phe element were found to be transcriptionally active in HeLa cell and Xenopus oocyte nuclear exts. The tRNAPhe gene transcripts were processed during the course of transcription to form mature-size tRNAPhe. The transcription efficiency of the B2Phe element was found to be an order of magnitude higher than that of the tRNAPhe gene. Competition expts. demonstrate that the B2Phe DNA can form a more stable transcription complex than the tRNAPhe gene and compete with it for binding of transcription factors.

IT 121293-42-3, Deoxyribonucleic acid (rat clone prB2Phe B2 element)

RL: PPE (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 121293-42-3 CAPLUS

CH DNA (rat clone prB2Phe B2 element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 ggggctagag agatggctca gcggttaaga gcaatggctg ctcttcaga
51 ggtcgtgagt tcaattccca gaaaccacat gacagctcac aaccataatg
101 ggttttgtgt ctcagaacct gagaaggcca ttgtcaagaa gtgagtgaga
151 aaggttaagt taggtggagt tgggccacct gcagagggtc tgtgtacaca
201 aaggttattt gtttgtggac aaggatatcc actgt

USJ ANSWER 20 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

AN 121293-42-3 CAPLUS

DN 121293-42-3

TI Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the entire nitrogen fixation gene cluster of *Klebsiella pneumoniae*

AU Arnold, Walter; Rump, Andreas; Klipp, Werner; Priefer, Ursula B.; Puehler, Alfred

CS Pat. Biol., Univ. Bielefeld, Bielefeld, D-4800/1, Fed. Rep. Ger.

SO Journal of Molecular Biology (1988), 203(3), 715-38

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CATEN: JMOBAK; ISSN: 0022-2736

DT Journal

LA English

AB The complete nucleotide sequence (24,206 base-pairs) of the *K. pneumoniae* gene region for nitrogen fixation (*nif*) is presented. Coding regions corresponding to the 19 known *nif* genes (including *nifW* and *nifZ*) could be identified. An addnl. open reading frame of 216 base-pairs, called *nifT*, was detected between *nifK* and *nifY*. Search for transcriptional signal structures revealed some unusual features: (1) several possible NifA-binding motifs are present in the intergenic regions between *nifJ* and *nifH* as well as between *nifX* and *nifU*; (2) a perfect NifA-binding motif, preceding the *nifENX* promoter, is located within an inverted repeat structure; (3) structures resembling the consensus *nif* promoter are found within the coding regions of *nifW* and *nifZ* and, together with a NifA-binding motif, in *nifN*. Typical rho-independent termination structures were detected only downstream from the *nifHDKTY* and the *nifBQ* operons. Anal. of the deduced amino acid sequences revealed the presence of two Cys-X2-Cys-X2-Cys-X3-Cys-Pro clusters in the pyruvate-flavodoxin

STN Columbus

oxidoreductase NifJ. This arrangement of cysteine residues is normally present only in ferredoxins. A high degree of homol. between the 2 gene products (NifE and NifN) involved in iron-molybdenum cofactor biosynthesis and the 2 nitrogenase component I structural proteins (NifD and NifK) was found. All four proteins are characterized by the conserved motif His-Gly-X2-Gly-Cys, which may play a role in binding the iron-molybdenum cofactor.

IT 120946-05-6, Deoxyribonucleic acid (Klebsiella pneumoniae gene nifW)

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 120946-05-6 CAPLUS

CN DNA (Klebsiella pneumoniae gene nifW) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgatggagt ggttttatca aattcccggc gtggacgaac ttcgctccgc
51 cgaatctttt tttagtttt tcgccgtccc ctatcagccc gagctgcttg
101 gccgctgcag cctgccggtg ctggcaacgt ttcacgcaa actccgcgcg
151 gaggtgccgc tgcaaaaccg gctcgaggat aacgaccgcg cgccctggct
201 gctggcgcca agactgctcg cggagagcta tcagcaacag ttccaggaga
251 gcggaacatg a

L61 ANSWER 25 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

AN 120946-05-655 CAPLUS

DN 120946-05-6

TE 120946-05-6 nucleotide sequence of the nifT, nifY, nifX and nifW genes of K.

120946-05-6

AU 120946-05-6 Kim, Cannon, Maura; Buchanan-Wollaston, Vicky; Ally, Abdul;

120946-05-6 Analyst, Robert; Dean, Denis; Cannon, Frank

CS 120946-05-6 Int. Inc., Cambridge, MA, 02140, USA

SC 120946-05-6 Acids Research (1968), 16(20), 9860

CODES: BARHAD: ISSN: 0305-1048

DT 120946-05-6

LA 120946-05-6

AB 120946-05-6 nucleotide sequences of the nifT, nifY, nifX, and nifW from Klebsiella pneumoniae were detd. These genes are within operons in the nif cluster.

IT 120946-05-6, Deoxyribonucleic acid (Klebsiella pneumoniae gene nifW)

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 120946-05-6 CAPLUS

CN DNA (Klebsiella pneumoniae gene nifW) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgatggagt ggttttatca aattcccggc gtggacgaac ttcgctccgc
51 cgaatctttt tttagtttt tcgccgtccc ctatcagccc gagctgcttg
101 gccgctgcag cctgccggtg ctggcaacgt ttcacgcaa actccgcgcg
151 gaggtgccgc tgcaaaaccg gctcgaggat aacgaccgcg cgccctggct
201 gctggcgcca agactgctcg cggagagcta tcagcaacag ttccaggaga
251 gcggaacatg a

L61 ANSWER 26 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

STN Columbus

Full Text

AN 1989:151808 CAPLUS

DN 110:151808

TI Expression of a fibrinogen fusion peptide in Escherichia coli: a model thrombin substrate for structure/function analysis

AU Lord, Susan T.; Fowlkes, Dana M.

CS Med. Sch., Univ. North Carolina, Chapel Hill, NC, 27599-7525, USA

SO Blood (1989), 73(1), 166-71

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CODEN: BLOOAW; ISSN: 0006-4971

DT Journal

LA English

AB A vector was constructed which expressed a tripartite protein (tribrid) consisting of amino acids 1-50 of the fibrinogen A α chain followed by 60 amino acids of chicken collagen and the β -galactosidase protein from E. coli. Cell lysates run on SDS-polyacrylamide gels contained the predicted band of mol. wt. 125,000. The tribrid reacted with a monoclonal antibody, Mab-Y18, which recognizes the N-terminus of the A α chain. When cell lysates were incubated with thrombin, fibrinopeptide A was released. By including 1 heterogeneous oligonucleotide in the construction, plasmids were generated that encoded 3 specific amino acid substitutions. Surprisingly changing glycine-14 to valine did not alter thrombin cleavage, although recognition by Mab-Y18 was lost. Substitution of isoleucine for arginine-23 did not alter either thrombin cleavage of monoclonal recognition. Substitution of leucine for arginine-16 altered thrombin cleavage; unexpectedly, recognition by Mab-Y15 was not changed.

IT 018022-32-5P

RI: SPN (Synthetic preparation); PREP (Preparation)
(prepn. of)

RN 110793-32-5 CAPLUS

CS DNA: G-A-A-C-T-A-C-A-A-A-T-G-C-C-C-T-T-C-T-G-G-C-T-G-C-A-G-G) (9CI) (CA
(INDEX NAME)

WFF singlestranded

SEQ ...tactacaaat gcccttcctgg ctgcagg

LC1 ANSWER 27 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1989:52100 CAPLUS

DN 110:52100

TI The cDNA and derived amino acid sequences for human and bovine matrix Gla protein

AU Kiefer, Michael C.; Bauer, Diane M.; Young, Daru; Hermen, Kathleen M.; ...

CS Chiron Corp., Emeryville, CA, 94608, USA

CO Nucleic Acids Research (1988), 16(11), 5213

CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB The cDNAs for matrix Gla protein (MGP) of human and cattle bone were isolated and sequenced. The amino acid sequences of the precursor proteins encoded by the cDNAs were 84.5% homologous, and the human cDNA-coded precursor was 31.5% homol. to that of rat MGP precursor. Unlike previously detd. vitamin K-dependent protein structures, the MGPs from human and rat do not contain a propeptide that is cleaved at a basic-K-basic-basic amino acid processing motif within the substrate recognition sites for vitamin K-dependent glutamic acid γ -carboxylase.

STN Columbus

IT 118441-10-4, Deoxyribonucleic acid (ox protein MGP messenger

RNA-complementary)

RL: FRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 118441-10-4 CAPLUS

CN DNA (cattle protein MGP cDNA) (9CI) (CA INDEX NAME)

NTS doublestranded

SEQ 1 atgaagagccc tgctccttct ctccatcctg gctgccttgg ccgtggcagc
51 tctgtgttat gaatctcacg aaagcctgga atcctatgaa atcaatccct
101 tcattaacag gagaaacgct aacagcttta tatcaccaca acagagatgg
151 agagcaaaag cccaagagag aatccgagaa ctcaacaagc ctcaatacga
201 gctcaaccgg gaagcttgtg atgacttcaa actttgcgaa cgctatgcca
251 tgggtgatgg atacaatgct gcctacgacc gttatttccg gcagcgccga
301 ggggccaaat ga

L61 ANSWER 28 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1989:51984 CAPLUS

DN 110:51984

TI Colicin E8, a DNase which indicates an evolutionary relationship between
colicins E2 and E3

AU Toba, Kari; Masaki, Haruhiko; Ohta, Takahisa

CS Dep. Agric. Chem., Univ. Tokyo, Tokyo, 113, Japan

SO Journal of Bacteriology (1988), 170(7), 2237-42

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CODES JOEAAAY; ISSN: 0021-9193

COLICIN

Colicin

Colicin E8-J and its immunity protein were characterized with regard to
their activities and gene structures. Colicin E8 is a complex of protein
A and B. Protein A (the naked E8) exhibits an apparently nonspecific DNase
activity that is inhibited by protein B (the immunity protein), as in the
case of colicin E2. The nucleotide sequence of the downstream half of the
colicin operon of ColE8-J was detd. to be highly homologous to that of
ColE2-P9, with the exception of the hot spot region of the 3'-terminal
segment of the colicin gene and the adjacent immunity gene. The
immunity-like gene of ColE3-CA38 was, as assumed previously, extensively
homologous to the immunity gene of ColE8-J, and thus, ColE8-J was shown to be
situated between ColE2-P9 and ColE3-CA38 in the evolution of the E-group
Col plasmids.

IT 118280-05-6, Deoxyribonucleic acid (plasmid ColE8-J colicin E 8

lysis peptide gene lys)

RL: FRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 118280-05-6 CAPLUS

CN DNA (plasmid ColE8-J colicin E 8 lysis peptide gene lys) (9CI) (CA INDEX
NAME)

NTS doublestranded

SEQ 1 atgaaaaaaa taccagggat tattttattg cttcttcgac tcattattct
51 ggctgcatgt caggcaact atatccggga tggtcagggc gggaccgtat
101 tcccgctatc aacagctgaa gtgaccggat tagcaacgca gtaa

L61 ANSWER 29 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

STN Columbus

AN 1988:623655 CAPLUS
 DN 109:223655
 TI Nucleotide sequence and gene organization of sea urchin mitochondrial DNA
 AU Jacobs, Howard T.; Elliott, David J.; Math, Veerabhadracharya B.; Farquharson, Andrew
 CS Dep. Genet., Univ. Glasgow, Glasgow, G12 8QQ, UK
 SO Journal of Molecular Biology (1988), 202(2), 185-217

====

CODEN: JMOBAK; ISSN: 0022-2836
 DT Journal
 LA English
 AB The 15,650 base-pair mitochondrial genome of the sea urchin *Strongylocentrotus purpuratus* has been cloned and sequenced. It exhibits a novel organization that suggests the primary of post-transcriptional gene regulation. The same 13 polypeptides, 2 rRNAs and 22 tRNAs are encoded as in other animal mitochondrial DNAs, but are organized with extreme economy: non-coding information between genes is almost completely absent, some stop codons are generated post-transcriptionally and tRNA sequences are interspersed between only a minority of other structural genes. The genome uses a variant genetic code, in which AAA specifies asparagine, ATA isoleucine, TGA tryptophan, and AGN serine, and has an unusual pattern of codon bias. The order of genes show several differences from that of vertebrates. The genes for the large (16 S) rRNA and for NADH dehydrogenase subunit 41 (ND4L) are in different positions, located resp. between those encoding ND2 and cytochrome oxidase subunit I (COI) and between COI and COII. This organization is conserved amongst at least 4 regular echinoids diverging by some 225 million years. Most tRNA genes are also in different positions. The only long unassigned sequence in the genome (121 base-pairs) is located within a cluster of 15 tRNA genes. It contains elements resembling some of those found in the displacement (D) loop of vertebrate mtDNAs, notable polypurine-polypyrimidine tracts that may play a role in regulating transcription and the initiation of replication. The sepn. of the rRNA genes from each other and from the putative control region imposes special demands on the transcription of the genome.

IT 1988:623655

PRP (Properties); BSL (Biological study)
 (nucleotide sequence of)

AN 1988:623655 CAPLUS

DN DNA (Strongylocentrotus purpuratus clone lambda.mt1 reduced nicotinamide adenine dinucleotide dehydrogenase subunit 3 gene) (9CI) (CA INDEX NAME)

WEB doublestranded

SEQ 1 atgacaacta taatcttctt gtttagtata accattgcag tagccgtagt
 51 gcttggactg gctgacatg acccgactaa acgcaccagg gatagagaaa
 101 agagctcccc ctaccagtg ggttttgatc cgctaaaatc cgcccgatta
 151 cctttttcat tccggttttc tctgtcgcc attttgtttt agctgtttga
 201 cctagaaata gcaatgctct ctctttacc agctgtagg ctgataactc
 251 cccctccac cttaattcc atctcaatgg tttttatggg tatcttgaca
 301 ctcggattag tcttcgagt aataaaaagg ggctagaat gaggagagta
 351 a

L51 ANSWER 30 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1988:505710 CAPLUS

DN 109:105710

TI Sequence of cDNAs encoding subunit Vb of human and bovine cytochrome c

STN Columbus

oxidase
 AU Zeviani, Massimo; Sakoda, Saburo; Sherbany, Ariel A.; Nakase, Hirofumi;
 Rizzuto, Rosario; Samitt, Craig E.; DiMauro, Salvatore; Schon, Eric A.
 CS Coll. Physicians Surg., Columbia Univ., New York, NY, 10032, USA
 SO Gene (1988), 65(1), 1-11

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CODEN: GENED6; ISSN: 0378-1119

DT Journal

LA English

AB The authors isolated a full-length human fetal muscle cDNA clone specifying the nuclear-encoded subunit Vb of the human mitochondrial respiratory chain enzyme, cytochrome c oxidase (COX; EC 1.9.3.1), and a partial-length cDNA clone from brain specifying the analogous bovine subunit. The 2 cDNAs are 85% identical at the nucleotide level. Similar to other proteins imported into mitochondria, the deduced human COX Vb protein contains a presequence, 31 amino acids long, rich in basic residues. There was no evidence for tissue-specific transcripts for subunit Vb of human COX, as Northern anal. of total RNA for human muscle, liver, and brain showed a single, identically sized transcript in each cell type, whereas partial-length cDNA clones isolated from human muscle and endothelial cell cDNA libraries were identical in sequence to the fetal muscle cDNA.

IT 116243-65-3, Deoxyribonucleic acid (human clone HCOX5.21 cytochrome oxidase subunit Vb mRNA-complementary)
 RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)

RN 116243-65-3 CAPLUS

CN DNA (human clone HCOX5.21 cytochrome oxidase subunit Vb cDNA) (9CI) (CA
 (BIOLOGICAL NAME))

NT Doublestranded

SEQ
 1 tagcttcaa gggtacttcg gggagctgga acgctggccg cgcaggccct
 61 gagggtctgc ggccccagtg gcggggcgcg gatgcgtcc atggcatctg
 121 gagggtggtg tccactgat gaagagcagg cyactgggtt ggagagggag
 181 ctatgctgg ctgcaaaagaa gggaactggac ccatacatg tactggcccc
 241 aaaggaggct acaggcacca gggaagacc taatttagtc cctccatct
 301 caacaagag gatagtaggc ggcattctgtg aegaggacaa taccagcgtc
 361 gtctggtttt ggctgcacaa agggcagggc cagcgatgcc cccgctgtgg
 421 ggcaccattac aagctgggtgc cccagcagct ggcacactga

LET ANSWER 31 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

2001-2001

AN 1987-167910 CAPLUS

DN 1987-167910

TI Human cysteine-proteinase inhibitors: nucleotide sequence analysis of
 members of the cystatin gene family

AU Galpin, Eiichi; Kim, Hyung Suk; Smithies, Oliver; Maeda, Nobuyo

CS Lab. Gen., Univ. Wisconsin-Madison, Madison, WI, 53706, USA

SO Gene (1987), 61(3), 329-33

====

CODEN: GENED6; ISSN: 0378-1119

DT Journal

LA English

AB Three genes from the human cystatin gene family of cysteine-proteinase inhibitors were isolated from a phage λ library contg. HindIII digests of human genomic DNA. Two of the genes code for salivary cystatin SN and SA; the third is a pseudogene. The cloned genes were identified with a probe made from a salivary cystatin cDNA. The complete nucleotide

STN Columbus

sequence of the gene that codes for the precursor form of the neutral salivary protein, cystatin SN, was detd. The gene, which was named CST1, contains 3 exons and 2 intervening sequences. The expected CAT and ATA boxes are present in the 5'-flanking region of the gene. Partial nucleotide sequence detn. of a second gene revealed that it codes for the precursor form of the acidic salivary protein, cystatin SA. This gene, designated CST2, has the same gene organization as CST1. The complete nucleotide sequence of a 3rd gene was detd. It does not contain a typical ATA box, and in addn., a premature stop codon and a frameshift deletion mutation occur within the gene. These inactivation mutations show that this gene, designated CSTP1, is a cystatin pseudogene. These data combined with genomic Southern-blot analyses show that the cystatin genes form a multigene family with ≥ 27 members.

IT 115682-20-7, Decyribonucleic acid (human clone CSTP1 pseudogene CSTP1)

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 115682-20-7 CAPLUS

CN DNA (human clone CSTP1 pseudogene CSTP1) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgcccttc actctcctgc attccccct tctcactctt tgccttgc
51 ccagcagacc acaacctggc cctgcacac tccactgcc ttgctggctg
101 cccgttttgt ggcctagcc tag

L61 ANSWER 32 OF 52 CAPLUS COPYRIGHT 2005 ACS on STN

FALL 1994

AN 1985-268218 CAPLUS

DN 1985-268218

TI Human lysozyme and its manufacture and secretion with Saccharomyces

IN Chikara, Yoshifumi; Muraki, Michiro; Harada, Nobuhiro; Tanaka, Hideaki;

Imai, Satoshi

PA Agency of Industrial Sciences and Technology, Japan

SO Jpn Kokai Tokkyo Koho, 15 pp.

CODING: JXXXXX

DT Patent

LA Japanese

FAN: CPT1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 6348482	A2	19871029	JP 1985-268218	19851128
JP 6350474	A2	19911107		
JP 63180479	A2	19910803	JP 1990-332827	19901129
JP 63660916	A2	19930903		
PRAJ JP 1985-268218		19851128		

AB Human lysozyme (I) precursor composed of I and chicken I signal peptide is manufactured and secreted by Saccharomyces. The DNA sequence encoding I precursor, which sequence is composed of a synthetic DNA fragment coding for the signal peptide of chicken I and the structural gene coding for human I (isolated from pHLYS-1), was cloned into pHLYSIG. The SalI-HindIII fragment (800 basepair) of pHLYSIG contg. the fused sequence was subcloned into YEp51 contg. the GAL10 promoter to form the expression plasmid YEp-HLYSIG. S. cerevisiae KK4 (YEp-HLYSIG) cultivated by a conventional method secreted 60% of the I precursor into the medium (at stationary phase). The purified I precursor possessed bacteriolytic activity comparable to the com. I.

IT 114680-29-4

RL: PRP (Properties)

STN Columbus

(expression in *Saccharomyces cerevisiae* and nucleotide sequence of)
 RN 114680-29-4 CAPLUS
 CN DNA, d(A-T-G-A-G-G-T-C-T-T-T-G-C-T-A-A-T-C-T-T-G-G-T-G-C-T-T-T-G-C-T-T-C-C-T-G-C-C-C-T-G-G-C-T-G-C-T-C-T-G-G-G), complex with DNA
 d(C-C-C-C-A-G-A-G-C-A-G-C-C-A-G-G-G-C-A-G-G-A-A-G-C-A-A-A-G-C-A-C-C-A-A-G-A-T-T-A-G-C-A-A-A-G-A-C-C-T-C-A-T) (1:1) (9CI) (CA INDEX NAME)

SEQ 1 atgaggtctt tgctatctt ggtgcttgc ttctgcccc tggctgctct
 51 gggg

L61 ANSWER 33 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1938:107263 CAPLUS

DN 108:107263

TI Cloning and characterization of a novel T cell activation gene

AU Burd, Parris R.; Freeman, Gordon J.; Wilson, Stephen D.; Berman, Michael; DeKruyff, Rosemarie; Billings, Paul R.; Dorf, Martin E.

CS Dana-Farber Cancer Inst., Harvard Med. Sch., Boston, MA, 02115, USA

SO Journal of Immunology (1987), 139(9), 3126-31

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CODEN: JOIMA3; ISSN: 0022-1767

DT Journal

LA English

AB The technique of subtractive hybridization was used to identify a T cell gene selectively expressed during activation via the antigen-receptor pathway. This gene, termed TCA3 (for T cell activation), encodes a mRNA which is expressed following concanavalin A (Con A) activation of T cell clones at levels of approx. 1% total poly(A)-contg. mRNA. The cDNA isolate, termed TCA3.0, is 512 bases in length, excluding poly(A), and encodes a predicted 93-amino acid protein having the characteristics of a secreted polypeptide of approx. 69 amino acids. The genomic organization of TCA3 was detd. for two lambda phage clones and was found to be a single copy gene contg. at least three exons dispersed over less than 4.7 kb. The temporal appearance of TCA3 mRNA in response to several activating agents was examd. It is not transcribed in response to interleukin 2 stimulation, but is transcribed in response to either antigen or Con A stimulation and can be detected as early as 1 h poststimulation. Expression of TCA3 in response to Con A is blocked by cyclosporin A treatment. The combined data suggest that TCA3 may represent a new lymphokine.

IT 113314-69-5

XL PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)

RN 113314-69-5 CAPLUS

CN DNA (mouse clone TCA3.0 gene TCA3 glycoprotein cDNA) (9CI) (CA INDEX NAME)

SEQ 1 atgaaaccca ctgccatggc actgatgtgc ctgctgctgg ctgccgtgtg
 51 gatacaggat gttgacagca agagcatgct tacgggtctcc aatagctgct
 101 gcttgaacac cttgaagaaa gagctcccc tgaagtttat ccagtgttac
 151 agaaagatgg gctctctctg tctgatccc ccagctgtgg tattcaggct
 201 gaacaaaggt agagaaagct gcgcctcaac taacaaaacg tgggttcaaa
 251 atcacctgaa gaaggtgaac ccttgctaa

STN Columbus

L61 ANSWER 34 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1988:107262 CAPLUS

DN 108:107262

TI Human acidic ribosomal phosphoproteins P0, P1, P2: analysis of cDNA clones, in vitro synthesis, and assembly

AU Rich, Benjamin E.; Steitz, Joan A.

CS Sch. Med., Yale Univ., New Haven, CT, 06510-8024, USA

SO Molecular and Cellular Biology (1987), 7(11), 4065-74

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CODEN: MCEBD4; ISSN: 0270-7306

DT Journal

LA English

AB The cDNA clones encoding three antigenically related human ribosomal phosphoproteins (P-proteins) P0, P1, and P2 were isolated and sequenced. P1 and P2 are analogous to Escherichia coli ribosomal protein L7/L12, and P0 is likely to be an analog of L10. The three proteins have a nearly identical C-terminal 17-amino-acid sequence (KEESEESD(D/E)DMGFGLFD-COOH) that is the basis of their immunol. cross-reactivity. The identities of the P1 and P2 cDNAs were confirmed by the strong similarities of their encoded amino acid sequences to published primary structures of the homologous rat, brine shrimp, and Saccharomyces cerevisiae proteins. The P0 cDNA was initially identified by translation of hybrid-selected mRNA and immunopptn. of the products. To demonstrate that the coding sequences are full length, the P0, P1, and P2 cDNAs were transcribed in vitro by bacteriophage T7 RNA polymerase and the resulting mRNAs were translated in vitro. The synthetic P0, P1, and P2 proteins were serol. and electrophoretically identical to P-proteins extd. from HeLa cells. These synthetic P-proteins were incorporated into 60 S but not 40 S ribosomes and also assembled into a complex similar to that described for E. coli L7/L12 and L10.

DE 108:107262-3

AD 108 (Properties); BIOL (Biological study)
nucleotide sequence of)

DE 108:107262-3 CAPLUS

CA 108 (human clone pTVP2 phosphoprotein P 2 cDNA) (9CI) (CA INDEX NAME)

```

550      1 atgcgctacg tcgctccta cctgctggct gccctagggg gcaactctc
      51 cccagcgcc aaggacatca agaagatctt ggacagcgtg ggtatcgagg
     101 cggacgacga cgggctcaac aaggttatca gtgagctgaa tggaaaaaac
     151 attgaagacg tcattgccca gggatttggc aagcttgcca gtgtacctgc
     201 tgggtggggct gtagccgtct ctgctgcccc aggctctgca gccctgctg
     251 ctggttctgc ccctgctgca gcagaggaga agaaagatga gaagaaggag
     301 gagtctgaag agtcagatga tgacatggga tttggccttt ttgattaa
  
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L61 ANSWER 35 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1988:107171 CAPLUS

DN 108:107171

TI Nucleotide sequences from the colicin E8 operon: homology with plasmid ColE2-P9

AU Uchiwara, Tai; Lau, Peter C. K.

CS Div. Biol. Sci., Natl. Res. Coun. Canada, Ottawa, ON, K1A 0R6, Can.

SO Molecular and General Genetics (1987), 209(3), 489-93

====

CODEN: MGGEAE; ISSN: 0026-8925

DT Journal

LA English

STN Columbus

AB The primary structures of the immunity (Imm) and lysis (Lys) proteins, and the C-terminal 205 amino acid residues of colicin E8 were deduced from nucleotide sequencing of the 1265-bp ClaI-PvuI DNA fragment of plasmid ColE8-J. The gene order is col-imm-lys confirming previous genetic data. A comparison of the colicin E8 peptide sequence with the available colicin E2-P9 sequence shows an identical receptor-binding domain but 20 amino acid replacements and a clustering of synonymous codon usage in the nuclease-active region. Sequence homol. of the 2 colicins indicates that they are descended from a common ancestral gene and that colicin E8, like colicin E2, may also function as a DNA endonuclease. The native ColE8 imm (resident copy) is 258-bp long and is predicted to encode an acidic protein of 9604 mol. wt. The 6 amino acid replacements between the resident imm and the previously reported non-resident copy of the ColE8 imm ([E8 imm]) found in the RNase-producing ColE3-CA38 plasmid offer an explanation for the incomplete protection conferred by [E8 Imm] to exogenously added colicin E8. Except for 1 nucleotide and amino acid change in the putative signal peptide sequence, the ColE8 lys structure is identical to that present in ColE2-P9 and ColE3-CA38.

IT 113256-05-6

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 113256-05-6 CAPLUS

CN DNA (plasmid ColE8-J colicin E 8 lysis peptide gene lys) (9CI) (CA INDEX NAME)

ITE doublestranded

SEQ 1 atgaaaaaaa caacagggat tattttatgt cttctgcag tcactattct
51 aggtgcatgt caggcaact atatccggga tgttcagggc eggaccgtat
101 atccgtcatc aacagctgaa gtgaecggat tagcaacgca gtaa

561 113256-05-6 OF 52 CAPLUS COPYRIGHT 2005 ACS on STN

ENGLISH

AF 1986-03-19 CAPLUS

DI 1986-03-19

TI Molecular cloning of matrix Gla protein: implications for substrate recognition by the vitamin K-dependent γ -carboxylase

AU Price, Paul A.; Fraser, James D.; Metz-Virca, Gabrielle

CS Dep. Biol., Univ. California, San Diego, La Jolla, CA, 92093, USA

SO Proceedings of the National Academy of Sciences of the United States of America (1987), 84(23), 8335-9

====

COLON: PNACA5; ISSN: 0027-8424

DT Source

LA English

AB Matrix Gla protein (MGP), a low mol. wt. protein found in bone, dentin, and cartilage, contains 5 residues of the vitamin K-dependent amino acid γ -carboxyglutamic acid (Gla). Antibodies raised against MGP and oligonucleotide probes were used to screen a λ gt11 cDNA library constructed from the rat osteosarcoma cells (line ROS 17/2) that had been pretreated with 1 α ,25-dihydroxyvitamin D3. By sequencing several cloned cDNAs, a 523-base-pair sequence that predicts an 84-residue mature MGP and a 19-residue hydrophobic signal peptide was established. The 84-residue mature rat MGP predicted from the cDNA sequence has an addnl. 5 residues at its C terminus (-Arg-Arg-Gly-Ala-Lys) not seen in the sequence of MGP isolated from bovine bone. The structure of rat MGP provides insight into the mechanisms by which the vitamin K-dependent γ -carboxylase recognizes substrate. The present studies show that MGP, unlike other vitamin K-dependent proteins, lacks a propeptide. The

STN Columbus

absence of an MGP propeptide demonstrates that γ -carboxylation and secretion of vitamin K-dependent proteins need not be linked to the presence of a propeptide or to its proteolytic removal. The propeptides of other vitamin K-dependent proteins are structurally homologous, and there is evidence that this homologous propeptide domain is important to substrate recognition by the γ -carboxylase. Mature MCP has a sequence segment (residues 15-30) that is homologous to the propeptide of other vitamin K-dependent proteins and probably serves the same role in γ -carboxylase recognition. Rat MGP also has a second sequence that has recently been identified in all known vitamin K-dependent vertebrate proteins, the invariant unit Glu-Xaa-Xaa-Xaa-Glu-Xaa-Cys (EXXXEXC). Since the glutamic residues in this unit are sites of γ -carboxylation, it has been suggested that the EXXXEXC unit could allow the γ -carboxylase to discriminate between substrate and product. The demonstration that 2 structures common to vitamin K-dependent proteins, the homologous propeptide domain and the invariant EXXXEXC unit, are in mature MGP indicates that des- γ -carboxy-MGP should be an excellent *in vitro* γ -carboxylase substrate for anal. of mechanisms involved in substrate recognition and product disson.

IT 113014-36-1

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 113014-36-1 CAPLUS

RN 113014-36-1 CAPLOS
 CN DNA (rat clone λ MGP-6/ λ MGP-1 protein MGP cDNA) (9CI) (CA
 INDEX NAME)

NTE doublestranded

```

590      tggaaagcgcc  tgcctccctct  ggccatccctg  gctgcgcgtgg  cegtggcagc
591      ctgtgtgtat  gaatctcacg  aaagcatgga  atcctatgaa  gtcagtcctt
592      tttaccaacgg  gagaaatgcc  aacaccttta  tatccctcca  gcagagatgg
593      ctgcgctaagg  cccacgaaag  agtcggggaa  ctcaacaagc  ctgcccagga
594      gttcaacagg  gaggcctgtg  atgactacaa  gctgtgtcag  cgctacgcc
595      tctctacgg  gtacaacgcs  gctacaanc  gctacttcag  gcagcgccga
596      ttggccaaat  aa

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661 ANSWER 37 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text:

1958-50148 CAPLUS

DN: 2.2B 5.248

11 Cloning and sequencing of the HU-2 gene of Escherichia coli

11 Kano, Yasunobu; Osato, Katsuaki; Wada, Morimasa; Imamoto, Fumio

CS Lab. Mol. Genet., Inst. Phys. Chem. Res., Yatabe, 305, Japan

80. Molecular and General Genetics (1987), 209(2), 408-10

CODEN: MEGEAE; ISSN: 0026-8925

DE

English

AB The HU-2 gene was cloned using a DNA fragment from the HU-1 gene as a probe. The amino acid sequence of the HU-2 protein deduced from the nucleotide sequence is in good agreement with the published sequence. The nucleotide sequence has a possible promoter and a typical ribosomal binding site upstream of the translation initiation codon (AUG) and a possible rho-independent terminator site downstream of the termination codon (UAA) of the gene.

IT 112353-29-4

XL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 112353-29-4 CAPLUS

STN Columbus

CN DNA (Escherichia coli gene HU-2) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaacaaga ctcaactgat tgatgtaatt gcagagaaag cagaactgtc
51 caaaaccag gctaaagctg ctctggagtc cactctggct gcaattactg
101 agtctctgaa agaaggcgat gctgtacaac tggttggtt cggtaccttc
151 aaagtgaacc accgcgctga gcgtactggc cgcaaccgc agaccggtaa
201 agaaatcaaa attgccgcag ctaacgtacc ggcatttgtt tctggcaagg
251 cactgaaaga cgcagttaag taa

L61 ANSWER 38 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text:

AN 1987:612642 CAPLUS

DN 107:212642

TI Cloning, DNA sequence, and expression of the Rhodobacter sphaeroides light-harvesting B800-850- α and B800-850- β genes

AU Kiley, Patricia J.; Kaplan, Samuel

CS Dep. Microbiol., Univ. Illinois, Urbana, IL, 61801, USA

SO Journal of Bacteriology (1987), 169(7), 3268-75

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CODEN: JOBAAY; ISSN: 0021-9193

DT Journal

LA English

AB Two deoxyoligonucleotide probes were synthesized in accordance with the available amino acid sequence of the B800-850- β polypeptide from R. sphaeroides and were used to isolate a 2.6-kilobase PstI fragment from R. sphaeroides 2.4.1 chromosomal DNA. Identification of the B800-850- β and B800-850- α structural genes, pucB and pucA, was confirmed by DNA sequencing. Northern (RNA) blot anal., using restriction endonuclease fragments from the cloned genes as probes, revealed a single pucB-pucA-specific, highly stable transcript of approx. 640 bases present in photosynthetically grown cells. In vitro transcription-translation analysis of the puc operon revealed that the max. synthesis of the puc operon gene products was achieved when the entire 2.6-kilobase PstI fragment was used as the template, although a 537-base-pair XmaIII fragment was sufficient to direct the synthesis of pucB and a pucA fusion product.

IT 100:70-51-6

RI: PUC (Properties); BIOL (Biological study)
Nucleotide sequence of)

RN 100:70-51-6 CAPLUS

CN DNA (Rhodobacter sphaeroides strain NCIB 8253 clone pMA81 gene pucA) (9CI)
(CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaccaacg gcaaaatctg gctcgtggtg aaaccgaccg tcggcggttc
51 gctgttcttc agcgctgcgc tcatcgcttc cgctgttacc cagctgctg
101 tcttgacgac caccacctgg ctgccgcct actaccaagg ctgggctgcg
151 ctgcggcgcc agtaa

L61 ANSWER 39 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text:

AN 1987:592060 CAPLUS

DN 107:192060

TI Observations on the structure of two human 7SK pseudogenes and on

STN Columbus

homologous transcripts in vertebrate species
 AU Humphries, Peter; Russell, S. E. Hilary; McWilliam, Peter; McQuaid,
 Shirley; Pearson, Colin; Humphries, Marian M.
 CS Dep. Genet., Trinity Coll., Dublin, Ire.
 SO Biochemical Journal (1987), 245(1), 281-4

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CODEN: BIJOAK; ISSN: 0306-3275
 DT Journal
 LA English
 AB A comparison of the sequence of 2 human 7SK RNA pseudogenes, covering approx. 190 and 240 base-pairs of the structural gene, is presented. Both repeated elements are flanked by direct repeats and begin at the 5' end of the gene. Each terminates approx. 90 base-pairs short of the 3' end, the latter representing a contiguous sequence and the former carrying an internal deletion of 40 base-pairs, this region being flanked in the progenitor gene by short repeated sequences. Southern blotting using a human 7SK pseudogene probe illuminated a series of multiple restriction fragments in mammalian genomes, with generally fewer fragments in the genomes of birds and reptiles and a single reactive fragment in DNA from terrapin (*Pseudemys scripta elegans*) and *Xenopus laevis* (Scuth African clawed toad). In the latter case, this fragment was only detectable on long exposure under the hybridization stringencies employed. 7SK transcripts were readily detectable in all mammalian, avian, reptilian, and amphibian species analyzed, although the gene appeared to be expressed at rather low levels in the ovaries of *Xenopus laevis*, possibly accounting for its failure to have become dispersed via retroposition in this species.

IT 110441-25-0

REL: PPE (Properties); BIOL (Biological study)
 (nucleotide sequence of)

RN 110441-25-0 CAPLUS

CM DNA (human RNA 7-3 pseudogene A) (9CI) (CA INDEX NAME)

NFE Unpublished

230 1 AAGGAGGGG aatctggtg cgacatctgt cccactgat taccagggtt
 51 gattcgctg atctggtg ctaggggggt ctctcttcc tccctcagcc
 131 ctgcattgt gtacctctg aagcgactg gtcttcagtc aagggtagac
 151 gctagctgt gctccctgc tagaacctcc aaacaagtc tcaagaagga
 201 gctatttag

L61 NUMBER 10 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Enl Tag

AN 110441-25-0 CAPLUS

DN 107-110762

TI Structural and functional analysis of a human 7 S K RNA gene

AU Kasper, Winfried; Benecke, Bernd Joachim

CS Dept Biochem., Ruhr-Univ., Bochum, D-463/1, Fed. Rep. Ger.

SO Journal of Molecular Biology (1987), 195(1), 31-41

====

CODEN: JMOBAK; ISSN: 0022-2836

DT Journal

LA English

AB Using purified RNA from HeLa cells, a cDNA encoding an almost entire 7 S K RNA was cloned and sequenced. This cDNA probe was used to isolate 7 S K RNA gene sequences from a human genomic library by high-stringency colony hybridization. In order to differentiate between functional genes and related sequences, a rapid in vitro transcription assay of purified phage DNA was used. With this addnl. screening criterion applied to selected

STN Columbus

clones, one recombinant phage was obtained that contained a complete 7 S K RNA gene and, immediately adjacent to its 3' end, a truncated pseudogene. The nucleotide sequence of both genes including the flanking regions has been detd. The functional integrity of the isolated 7 S K RNA gene was verified by in vitro transcription studies with cell-free exts. and by fingerprinting of the specific transcripts with RNase T1. Under optimal ionic conditions, the transcription efficiency in vitro of this 7 S K RNA gene was found to be comparable to that of a human 7 S L RNA gene. A series of 5'-deletion mutants showed that transcription of 7 S K RNA in vitro depends on 5'-flanking sequences. The region up to position -67 was detd. to be essential for efficient transcription in vitro of 7 S K RNA. While apparently a variety of 7 S K related sequences is distributed within the human genome, hybridization of 5'-flanking sequences to genomic DNA revealed that possibly not more than one copy of this gene is present per haploid genome.

IT 110735-47-2

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 110735-47-2 CAPLUS

CN DNA (human clone p9.1 7-3 RNA gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 ggatgtgagg cgatctggct ggcacatctg tcacccatt gatcgccagg
50 gttgattcgg cggatctggc tggctaggcg ggtgtcccct tctccctca
100 cggctccatg tgcgtccctc cgaagctgc gcgctcggtc gaagaggacg
150 atcatccccc atagaggagg accggtcttc ggtcaagggt atacgagtag
200 ctgcgctccc ctgctagaac ctccaaacaa gctctcaagg tccatttgta
250 ggcgaacgta gggtagtcac gcttccaaga ctgcagacac atccaatga
300 ggcgctycat gtggcagttt gctttcttt t

LSL ANSWER 11 OF 52 CAPLUS COPYRIGHT 2005 ACS on STN

11-1-1986

AN 1571564524 CAPLUS

EN 1571564524

TI Cloning and oxygen regulated expression of genes coding for the reaction center and light harvesting polypeptides of Rhodospseudomonas sphaeroides

AU Ashby, Mark K.; Croomer, Shirley A.; Hunter, C. Neil

CS Dep. Pure Appl. Biol., Imp. Coll. Sci. Technol., London, SW7 2BB, UK

SC Proc. Photosynth. Res., Proc. Int. Congr. Photosynth., 7th (1987),

====

Meeting Date 1986, Volume 4, 733-6. Editor(s): Biggins, John. Publisher: Nijhoff, Dordrecht, Neth.

CODEN PSERQAT

DT Conference

LA English

AB In *R. sphaeroides*, the light harvesting app. contains 3 pigment-protein complexes: B800-850, B875, and the reaction center. Cloned gene probes were used to study the levels of transcripts for these proteins in cells induced to pigment. The genes for the reaction center and B875 are co-regulated, with a peak of transcription at 50-90 min after induction. The B800-850 apoprotein gene is encoded on 2 transcripts, 2.6 and 0.5 kb; the 2.6 kb message also encodes the reaction center. The nucleotide sequence of the B800-850 genes was detd. The B800-850 genes are transcribed on one 0.5 kb transcript; the level of mRNA does not reach a peak until 6 h after pigment induction.

IT 109370-10-6

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

STN Columbus

RN 109370-51-6 CAPLUS
CN DNA (Rhodobacter sphaeroides strain NCIB 8253 clone pMA81 gene pucA) (9CI)
(CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaccaacg gcaaaatctg gctcgtggtg aaaccgaccg tcggcggtcc
51 gctgttccctc agcgctgccg tcatcgcttc cgctgttatt cagctgctg
101 tgctgacgac caccacctgg ctgcccgct actaccaagg ctgggctgag
151 gtcgcgccg agtaa

L61 ANSWER 42 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1037:453079 CAPLUS

DN 107:53079

TI Cloning, nucleotide sequence, and transfer of genes for the B800-850 light harvesting complex of Rhodobacter sphaeroides

AU Ashby, Mark K.; Coomber, Shirley A.; Hunter, C. Neil

CS Dep. Pure Appl. Biol., Imp. Coll., London, SW7 2BB, UK

SO FEBS Letters (1987), 213(2), 245-8

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CODEN: FEBLAL; ISSN: 0014-5793

DT Journal

LA English

AB Two genes that encode the α and β polypeptides of the major light-harvesting complex of R. sphaeroides, B800-850, were cloned and sequenced through the use of oligonucleotides based upon the known polypeptide sequences. These genes, pucA and B, are transcribed in the same B, A, are of 150 and 164 nucleotides resp., and are sepd. by a spacer region of 14 nucleotides. Transfer of these genes to mutant M21 lacking the B800-850 complex has been accomplished, and absorbance spectra of recombinant strains M2131 and M2184 show that expression of pucA and B is comparable to levels found in the wild type.

FE 1037:453079-5

FE FRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 109370-51-6 CAPLUS

CN DNA (Rhodobacter sphaeroides strain NCIB 8253 clone pMA81 gene pucA) (9CI)
(CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaccaacg gcaaaatctg gctcgtggtg aaaccgaccg tcggcggtcc
51 gctgttccctc agcgctgccg tcatcgcttc cgctgttatt cagctgctg
101 tgctgacgac caccacctgg ctgcccgct actaccaagg ctgggctgag
151 gtcgcgccg agtaa

L61 ANSWER 43 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1067:114518 CAPLUS

DN 1067:114518

TI cDNA sequences of two apolipoproteins from lamprey

AU Pontes, M.; Xu, X.; Graham, D.; Riley, M.; Doolittle, R. F.

CS Dep. Chem., Univ. California, San Diego, La Jolla, CA, 92093, USA

SO Biochemistry (1987), 26(6), 1611-17

====

STN Columbus

CODEN: BICHAW; ISSN: 0066-2960

DT Journal

LA English

AB The messages for two small, but abundant, apolipoproteins found in lamprey blood plasma were cloned with the aid of oligonucleotide probes based on amino-terminal sequences. In both cases, numerous clones were identified in a lamprey liver cDNA library, consistent with the great abundance of these proteins in lamprey blood. One of the cDNAs (LaL1) has a coding region of 105 amino acids that corresponds to a 21-residue signal peptide, a putative 8-residue propeptide, and the 76-residue mature protein found in blood. The other cDNA (LAL2) codes for a total of 191 residues, the first 23 of which constitute a signal peptide. The two proteins, which occur in the high-d. lipoprotein fraction of ultracentrifuged plasma, have amino acid compns. similar to those of apolipoproteins found in mammalian blood; computer anal. indicates that the sequences are largely helix-permissive. When the sequences were searched against an amino acid sequence data base, rat apolipoprotein IV was the best matching candidate in both cases. Although a reasonable alignment can be made with that sequence and LAL1, definitive assignment of the 2 lamprey proteins to typical mammalian classes was not made.

IT 106946-82-1

RE: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 106946-82-1 CAPLUS

CN ENA (Petromyzon marinus clone LAL1 lipoprotein cDNA) (9CI) (CA INDEX NAME)

NTC doublestranded

SEQ 1-ctgaagctcc acgtggctgc cctggcgact ctgcgccgtcg tctgcatcct
51-ggcggcaggg tccgagggccg cgcccaaggc gatgtccgac ccggccgtgg
101-ttaaggccca gctcttccce gaagccttct gggagagctt caagaatgtg
151-cccttggagt tcaagaagat ggtgcacggc ctgcagacct ccaacatcgg
201-ggagacgccc aagagccgtg acaccgacac ggtggccgtg ctgaccccg
251-ctccacagaa gacccgcgag aadgtcacca agatgtacca gytgtacgtg
301-gagttcaagg agcactag

L67 ANSWER 44 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987:97:156 CAPLUS

DI 1987:97:156

TI A sequence upstream from the coding region is required for the transcription of the 7SK RNA genes.

AU Murphy, Shona; Tripodi, M.; Melli, Marialuisa

CS Sclavo Res. Cent., Siena, Italy.

SO Nucleic Acids Research (1986), 14(23), 9243-60

====
CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB Two recombinant λ phages were isolated and characterized that contain sequences homologous to 7SK RNA and code for a RNA 330 nucleotides long in an in vitro transcription system. S1 mapping of the transcript shows that this RNA corresponds to the 7SK RNA obtained from human cells, indicating that the two recombinant phages contain genes coding for 7SK RNA. The transcription of these genes is polymerase III dependent. Sequences upstream from the start of transcription are essential for in vitro synthesis of 7SK RNA, suggesting that internal promoter elements, if present, are not sufficient to support the synthesis of 7SK RNA. A region

STN Columbus

of homol. with the upstream sequences of the genes for U6 RNA, 7SL RNA, and Bombyx mori alanine tRNA is found within 50 base pairs from the transcription start point. Within the homologous region a motif common to the four genes is a TATA-like box, placed at position -30 to -25 of the 7SK RNA gene, which is typical of the polymerase II promoter region.

IT 106907-39-5

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 106907-39-5 CAPLUS

CN DNA (human clone 7SK33 7-3 RNA gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 ggatgtgagg gcatctggc tgcgacatct gtcaccccat tgatcgccag
51 ggttgattcg gctgatctgg ctggctaggc ggggtgtccc ttcttccctc
101 accgctccat gtgcgtccct cccgaagctg cgcgctcggt cgaagaggac
151 gaccatcccc gatagaggag gaccggtctt cgggtcaaggg tatacgagta
201 gctgcgctcc cctgctagaa cctccaaaca agctctcaag gtccatttgt
251 aggagaacgt agggtagtca agcttccaag actccagaca catccaaatg
301 aggcgctyca tgtggcagtc tgcctttctt tt

LC1 ANSWER 45 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987:79526 CAPLUS

DN 1987:79526

TI Structure and expression of the human calcitonin/CGRP genes

AU Steenbergh, P. H.; Hoppenen, J. W. M.; Zandberg, J.; Visser, A.; Lips, C. J. M.; Jansen, H. S.

CS Inst. Mol. Biol., Utrecht, 3508 TB, Neth.

CO PNAS Letters (1986), 202(1), 97-103

====
CODEN: FEPLAL; ISSN: 0014-5723

LP Journal

LA English

AB The isolation of cDNA encoding a 2nd human calcitonin gene-related peptide (hCGRP-II) [98824-26-1] was previously reported. The isolation and characterization of the gene encoding hCGRP-II are described. This gene, designated CALC-II, is structurally closely related to the known CALC-I gene encoding human calcitonin (hCT) and hCGRP-I. In contrast to CALC-I, CALC-II does not seem to be alternatively expressed. The formation of a 2nd, hCT-like mRNA by differential splicing of CALC-II transcripts is unlikely in view of the structure of CALC-II, and could not be demonstrated in tissues known to express CALC-I and CALC-II.

IT 105474-34-8

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 105474-34-8 CAPLUS

CN DNA (human clone Cos2CALC-II gene CALC-II coding region) (9CI) (CA INDEX NAME)

SEQ 1 atgggtttcc ggaagttctc ccccttcttg gctctcagta tcttggtctc
51 gtaccaggcg ggcagcctcc aggcggcgcc attcaggtct gccctggaga
101 gtagcccaaga cccggccaca ctacagtaaag aggacgcgcg cctctgctg
151 gctgcactgg tgcaggacta tgtgcagatg aaggccagtg agctgaagca
201 ggagcaggag acacagggtc ccagctccgc tgcccagaag agagcctgca
251 acactgcccac ctgtgtgact catcggtgag caggcttgct gaggagatca
301 gggggcatgg tgaagagcaa ctctgtgccc accaatgtgg gttccaaagg
351 ctttggcagg cgccgcaggg accttcaagc ctga

STN Columbus

L61 ANSWER 46 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987:44684 CAPLUS
 DN 106:44684
 TI Nucleotide sequence of the tra YALE region from IncFV plasmid pED208
 AU Finlay, B. Brett; Frost, Laura S.; Paranchych, William
 CS Dep. Biochem., Univ. Alberta, Edmonton, AB, T6G 2H7, Can.
 SO Journal of Bacteriology (1986), 168(2), 990-8

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CODEN: JOBAAY; ISSN: 0021-9193

DT Journal

LA English

AB The pED208 plasmid is a 90-kilobase (kb) conjugative plasmid which is the derepressed form of F0 lac plasmid (IncFV). A 3.3-kb HindIII-PstI fragment from the pED208 plasmid was cloned and sequenced and was found to contain 4 open reading frames which were highly homologous to the traA, traL, traE, and traY gene products of the F plasmid. The pED208 traA pilin protein was 119 amino acids in length, consisting of a leader sequence of 55 amino acids and a mature pilin subunit of 64 residues. The leader sequence contained a hydrophobic region followed by a classic signal peptidase cleavage site (Ala-Ser-Ala-55). F and pED208 pilin proteins shared 27 conserved residues and had similar predicted secondary structures. The pED208 traA and traL genes were sepd. by a single base pair and no ribosome binding site preceded the traL gene. The pED208 traY gene contained an IS2 insertion element in orientation II 180 nucleotides (60 residues) upstream of the traY stop codon. This insertion of IS2 resulted in a predicted fusion peptide of 69 residues for traY which may provide the obsd. traY activity. Since IS2 is absent in the wild-type plasmid, F0 Lac, derepression and concomitant multiplication may be due to the insertion of IS2 providing constitutive expression of the pED208 tra operon.

RT 1987:44684

RL PRO (Properties); BIOL (Biological study)
 (nucleotide sequence of)

RN 1987:44684-4 CAPLUS

CN DNA plasmid pED208 gene traA (9CI) (CA INDEX NAME)

NTS doublestranded

SEQ 1 atgaatttat cctttgcaaa aggcggcctc cctgcgcctg taataaacccg
 51 agcatggcag tactgccaga tggcatggcg cgggtgtgacc agtaaaaaag
 101 cgggtgtcccg tctggctcgg ctgtctccgc tgctgttact cgggtgtggga
 151 agatattgcca gtgcacccga cctgctggcc gggggcaagg atgatgtgaa
 201 agccaccttc ggtgccgact cattcgtcat gatgtgtatc atcattgccg
 251 aactgattgt cgggtgtggc atgtatatcc gcaccaagaa cctgctgac
 301 ctgctgggcc tgggtgtggt taccgtcttc actaccgtcg gtcttacctt
 351 catcaaatga

L61 ANSWER 47 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:585044 CAPLUS

DN 105:585044

TI Isolation of the human gene for bone gla protein utilizing mouse and rat cDNA clones

AU Calaste, A. J.; Rosen, V.; Suecker, J. L.; Kriz, R.; Wang, E. A.; Wozney,

STN Columbus

J. M.

CS Genet. Inst., Inc., Cambridge, MA, 02140, USA
 SO EMBO Journal (1986), 5(8), 1885-90

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CODEN: EMJODG; ISSN: 0261-4189

DT Journal

LA English

AB cDNAs which encode bone gla protein (BGP, osteocalcin), an abundant γ -carboxylated protein of bone, have been cloned from rat and mouse osteosarcoma cell lines. DNA sequence anal. indicates that the cDNAs code for both the 50 (rat) or 46 (mouse) amino acids of the mature proteins and a 49 amino acid leader peptide. The leader peptide of each BGP includes the expected hydrophobic signal sequence and an apparent pro sequence. Although there is no homol. between the mature forms of BGP and the γ -carboxylated clotting factors, there is some homol. between their leader peptides. These cDNAs have been used to examine the modulation of BGP mRNA levels by osteoblastic cells in response to hormones. The cDNAs have also allowed isolation of the human BGP gene; anal. of this gene indicates the presence of 4 exons. Comparison of the exon structure of the BGP gene and the Factor IX (a γ -carboxylated clotting factor) gene suggests that the exons encoding the part of the leader peptides presumably directing γ -carboxylation arose from a common ancestral sequence.

IT 104646-24-4

RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)

RN 104646-24-4 CAPLUS

CN DNA (mouse osteocalcin cDNA) (9CI) (CA INDEX NAME)

NTE Doublestranded

SEQ 1 atgaggaccc tctctctgct cactctgctg gccctggctg cgctctgtct
 2 cctggacctc acagatccca agcccagcgg ccttgagtct gacaaagcct
 3 tctgggtccaa gcaggagggc aataaggtag tgaacagact ccggcgctac
 4 tctggagcct cagtcgccag ccagatccc ctggagccca cccgggagca
 5 cctggagcct aacctgctt gtgacgagct accagaccag tatggcttga
 6 tgaacgccta caaacgcata tacggtatca ctatttag

L61 ANSWER 48 OF 52 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986-0086 CAPLUS

DN 1986-0086

TE Viral enhancer DNA segments

IN Coe, Eiichi, Yoshimura, Hiromitsu

PA Taiho Pharmaceutical Co., Ltd., Japan

SO Eur. Pat. Appl. 33 pp.

CODEN: EPXZDW

DT Patent

LA English

FAN. CMT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 154566	A2	19850911	EP 1985-301617	19850308 <--
	EP 154565	A3	19851030		
	EP 154566	B1	19900530		
	AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
	JP 60138075	A2	19850925	JP 1984-44437	19840308 <--
	JP 67089930	B4	19951004		
	US 4722897	A	19880202	US 1985-709281	19850307 <--

STN Columbus

AT 53237 E 19900615 AT 1985-301617 19850308
 PRAI JP 1984-44437 A 19840308
 EF 1985-301617 A 19850308

AB Enhancer elements are isolated from papovavirus BK mutants and are used to enhance the expression of cloned genes in host eukaryotic cells. Thus, viral DNAs were extd. from papovavirus BK mutants pm525, pm411, and pm522, and the HindIII-C fragment of each mutant was isolated, cloned into the phage vector mp8, and sequenced. The enhancer activity of each HindIII-C fragment was established by cloning the fragment into a plasmid pBR322 that already contains the herpes simplex type 1 virus thymidine kinase (TK) [9002-06-6] gene, plasmid pTK. The recombinant plasmids were introduced into mouse L (TK-) cells, and their expression was monitored. As a result, the HindIII-C DNA fragments of pm411, pm522, and pm525 viral DNAs showed 10.1-20-fold enhancement of transcription in mouse L (TK-) cells over the control. This activity was exhibited irresp. of the orientation, distance, or position of the HindIII-C DNA fragment.

IT 99533-39-7 99533-39-8 99533-40-1

RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)

RN 99533-39-7 CAPLUS

CN DNA (BK virus strain pm411 enhancer element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 cctttgtcca gtttaactat taactgccac tggctgctgc ccagtcacgc
 51 cctttccttc ctgaggtcat ggctggctgc ccagtcacgc actttccttc
 101 ttgagggctg ccagtcacat ctgaggtcat ggctggctgc ccagtcacgc
 151 cctttccttc ctgagggctg ccagtcacat cactttcctt cctgaggtca
 201 tgggttggtt gcattccatg gtaagcagc tcttcctgt gg

RN 99533-39-8 CAPLUS

CN DNA (BK virus strain pm522 enhancer element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 cctttgtcca gtttaactat taactgccac tggctggctg ccagtcacgc
 51 cactttcctt cctgaggtca tggctggctg ccagtcacgc cactttcctt
 101 cctgagggct gccagtcac gcactttcct tcttgagggc atggtttggc
 151 tgcattccat gggtagcag ctcctcctg tgg

RN 99533-40-1 CAPLUS

CN DNA (BK virus strain pm525 enhancer element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 cctttgtcca gtttaactat taactgccac tggctggctg ccagtcacgc
 51 cactttcctt cctgaggtca tggctggctg ccagtcacgc cactttcctt
 101 tgcacagttt taactttaac tgccactggc tggctgccct agtcacgcac
 151 tttccttctt gagggctgcc tagtcacgca ctttccttcc tgaggtcatg
 201 gtttggtgc attccatggg taagcagctc ctcctgtgg

L61 ANSWER 49 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:15341 CAPLUS

DN 104:15341

STN Columbus

TI DNA sequence and characterization of the Escherichia coli serB gene
 AU Neuwald, Andrew F.; Stauffer, George V.
 CS Dep. Microbiol., Univ. Iowa, Iowa City, IA, 52242, USA
 SO Nucleic Acids Research (1985), 13(19), 7025-39

====

CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB The sequence of a DNA fragment contg. the E. coli serB gene was detd. An open reading frame of 966 nucleotides was identified that encodes a polypeptide of 322 amino acids with a mol. wt. of 35,002 daltons. The transcription start site was detd. by Mung Bean nuclease mapping. The -10 and -35 regions of the serB promoter lack homol. to the consensus sequences. In addn., the -35 region of the serB promoter overlaps the -35 region of a 2nd divergent promoter. Frameshift mutations were constructed at 3 different sites within the serB gene. When plasmids carrying these mutations were used as templates in a minicell system, mutations closer to the proposed transcription and translation start sites resulted in smaller polypeptides than did those further away, confirming the proposed direction of transcription and translation. The obsd. sizes of the truncated and native polypeptides were in agreement with those predicted from the DNA sequence. A very stable stem and loop structure ($\Delta G = -32$ kcal/mol) that does not fit the criteria of known transcription terminators was found one nucleotide downstream from the putative UAA translation stop codon.

RT 99549-64-1

RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence)

REF 99549-64-1 CAPLUS

EN DNA (Escherichia coli clone pGS154 gene serB) (9CI) (CA INDEX NAME)

MT doublestranded

SEQ 1 atgcctaaca ttacctgggtg cgacctgcct gaagatgtct ctttatggcc
 51 gggctctgct ctttcartaa gtggctgatga actgatgccca ctggattacc
 101 acgcaggtcg tagcggctgg ctgctgtatg gtcgtgggct ggataaacia
 151 cgtctgaacc aataccagay caaactgggt gcggcgatgy tgattgttgc
 201 cgcctggtgc gtgggaagatt atcaggtgat tcgtctggca ggtrcactca
 251 cgcacagggc taacgcctg gccacgaag cgcagctgga tgtggcccg
 301 ctggggaaaa tcccgcacct gcgcacgccg cgggtttgct ggtga-

161 ANSWER 50 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:499559 CAPLUS

EN 103:99559

TI Structure of the Escherichia coli S10 ribosomal protein operon

AU Zurawski, Gerard; Zurawski, Sandra-Marvo

CS DNAX Res. Inst. Mol. Cell. Biol., Palo Alto, CA, 94304, USA

SO Nucleic Acids Research (1985), 13(12), 4521-6

====

CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB The complete structure of the E. coli S10 ribosomal protein operon is presented. Based on the DNA sequence, the deduced order of the 11 genes in the operon is rpsJ, rplC, rplD, rplW, rplB, rpsS, rplV, rpsC, rplP, rpsC, rpsQ. The estd. transcribed length of the operon is 5181 base pairs. Putative sequences involved in ribosome binding are discussed. The DNA sequence data corrects several errors in previously detd. protein

STN Columbus

sequence data.

IT 80451-23-6

RL: PRP (Properties)

(nucleotide sequences of)

RN 80451-23-6 CAPLUS

CN DNA (Escherichia coli ribosome protein S 10 gene) (9CI) (CA INDEX NAME)

SEQ 1 atgcagaacc aaagaatccg tatccgcctg aaagcgtttg atcatcgctt
51 gatcgatcaa gcaaccgcgg aaatcgctga gactgccaaag cgcactgggtg
101 cgcagggtccg tggctccgatc ccgctgccga cagcгааага gcgcttcact
151 gttctgatct ccccgacagt caacaaagac gcgcgcgatc agtacgaaat
201 ccgtactcac ttgcgtctgg ttgacatcgt tgagccaacc gagaaaaccg
251 ttgatgctct gatgcgtctg gatctggctg ccggtgtaga cgtgcagatc
301 agcctggggt aa

L61 ANSWER 51 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:482528 CAPLUS

DN 103:82528

TI Nucleotide sequence of the alpha ribosomal protein operon of Escherichia coli

AU Bedwell, David; Davis, Geneva; Gosink, Mark; Post, Leonard; Nomura, Masayasu; Kestler, Harry; Zengel, Janice M.; Lindahl, Lasse

CS Knoch. Enzyme Res., Univ. Wisconsin, Madison, WI, 53706, USA

SC Nucleic Acids Research (1985), 13(11), 3891-903

====
CODEN: NARHAD; ISSN: 0305-1043

DT Journal

LA English

AB The E. coli genome contains some 19 transcription units encoding the 52 ribosomal proteins. These are scattered throughout the genome. One of the units, the alpha operon, encodes genes for the ribosomal proteins S13, S11, S4, and L17 as well as the kilobase subunit of RNA polymerase. [9014-24-8]. The complete 4.3-kilobase nucleotide sequence of the alpha operon is reported. In addition, the site of transcription termination in this operon was detd.

IT 57708-10-6

RL: PRP (Properties); BIOL (Biological study)

(nucleotide sequence of)

RN 57708-10-6 CAPLUS

CN DNA (Escherichia coli ribosome protein S 13 gene) (9CI) (CA INDEX NAME)

SEQ 1 gaggcccgta tagcaggcat taacattcct gatcataagc atgccgtaat
51 agcattaact tagatttatg gcgtcggcaa gaccggttct aaagccatcc
101 tggctgcagc gggtatcgct gaagatgta agatcagtg gctgtctgaa
151 ggacaaatcg acacgctgcg tgacgaagtt gccaaatttg tcgttgaaag
201 agatctgcgc cgtgaaatca gcatgagcat caagcgctg atggatcttg
251 ttgtctatcg cggtttycgt catcgctcgt gtctcccggt tcgcggtcag
301 cgtaccaaga ccaacgcacg taccgtaag ggtccgcgca aaccgatcaa
351 gaaataa

L61 ANSWER 52 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:432882 CAPLUS

DN 103:32882

STN Columbus

TI Alternative RNA processing events in human calcitonin/calcitonin gene-related peptide gene expression
 AU Jonas, Vivian; Lin, Chijen R.; Kawashima, Eric; Semon, Dominique; Swanson, Larry W.; Mermod, Jean Jacques; Evans, Ronald M.; Rosenfeld, Michael G.
 CS Sch. Med., Univ. California, La Jolla, CA, 92093, USA
 SO Proceedings of the National Academy of Sciences of the United States of America (1985), 82(7), 1994-8

====

CODEN: PNASA6; ISSN: 0027-8424
 DT Journal
 LA English
 AB Two mRNAs generated as a consequence of alternative RNA processing events in expression of the human calcitonin [9007-12-9] gene encode the protein precursors of either calcitonin or calcitonin gene-related peptide (CGRP) [83652-28-2]. Both calcitonin and CGRP RNAs and their encoded peptide products are expressed in the human pituitary and in medullary thyroid tumors. Apparently, both the calcitonin and CGRP exons arose from a common primordial sequence, suggesting that duplication and rearrangement events are responsible for the generation of this complex transcription unit.

IT 95827-33-7

RL: ERP (Properties); BIOL (Biological study)
 (nucleotide sequence of)

RN 95827-33-7 CAPLUS

CN DNA (human clone pCGRPH1 calcitonin gene-related peptide cDNA) (9CI) (CA INDEX NAME)

NN Doublestranded

```

580      1 aacggcttcc aaaagttctc ccccttctcg gctctcagca tcttggtcct
      51 gctgcaggca ggcagctccc atgcagcacc attcaggtct gccctggaga
      101 gacgccagc agaccggccc acgctcagtg aggacgaagc ggcctcctg
      151 cgggctgcac tgggtcagga ctatgtgcag atgaaggcca gtgagctgga
      201 gaggagcaa gagagagagg gctccagaat pattgcccag aagagagcct
      251 gacactgc caccgtgccc actcatcggc tggcaggctt gctgagcaga
      301 gaggggctg cgggtgaaga caactttgtg cccaccaatg tgggttccaa
      351 agcttttggc aggcacgga gggacttcca agcctga
  
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LET ANSWER-53 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 198511120 CAPLUS

DN 95827-33-7

TI Cloning and characterization of a mRNA-encoding rat preprosomatostatin

AU Amara, Christie L.; Minn, Carolyn D.; Deschenes, Robert; Magazin, Aguilon; Tavianini, Marie A.; Sheets, Mike; Collier, Kenneth; Weith, H. Lee; Aron, David C.; et al.

CS Dep. Biochem., Purdue Univ., West Lafayette, IN, 47907, USA

SO Journal of Biological Chemistry (1983), 258(14), 8781-7

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CODEN: JBCHA3; ISSN: 0021-9258

DT Journal

LA English

AB An undecanucleotide extended hybridization probe was used to screen a rat medullary thyroid carcinoma cDNA library for clones which contain preprosomatostatin [75037-28-4] sequences. The nucleotide sequence encoding rat preprosomatostatin is reported. The sequence of cDNA contains 67 nucleotides in the 3'-noncoding region, 84 nucleotides in the 5'-untranslated region, and 458 bases corresponding to the coding region. The mRNA codes for a somatostatin precursor of 116 amino acids (mol. wt.

STN Columbus

12,773). The preprosomatostatin has a sequence of hydrophobic amino acids at the N terminus, which is followed by a peptide of ~78 residues, which precedes somatostatin-14 [51110-01-1]. The amino acid sequences of rat and human preprosomatostatin differ by only 4 amino acid residues. Translation of rat poly(A) RNA in a rabbit reticulocyte cell-free system followed by immunopptn. with antisera directed against somatostatin-14 demonstrated the synthesis of a single protein of mol. wt. 15,000. Two proteins, of mol. wts. 14,000 and 15,000, are immunopptd. from a wheat germ cell-free translation mixt. Northern anal. of the somatostatin mRNA indicated that it is of ~850 nucleotides. Anal. of several medullary thyroid carcinomas demonstrated that 1 tumor, designated WF, had immunoreactive somatostatin-14 in concns. of 350 ng somatostatin-14/mg protein and somatostatin mRNA that represented 10% of the cellular poly(A) RNA. Cell lines derived from this tumor might provide an attractive system to investigate the regulation of somatostatin gene expression.

IT 36090-46-2

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 86090-46-2 CAPLUS

CN DNA (rat somatostatin cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgctgtcct gccgtctcca gtgcgcgctg gccgcgctct gcacgtcct
51 ggctttgggc ggtgtcaccg gggcgccctc ggaccccaga ctccgtcagt
101 ttctgcagaa gtctctggcg gctgccaccg ggaaacagga actggccaag
151 taattcttgg cagaactgct gtctgagccc aaccagacag agaacgatgc
201 cctggagcct gaggatrtgc cccaggcagc tgagcaggac gagatgaggc
251 agcgctgca gaggtctgcc aactcgaacc cagccatggc accccgggaa
301 agcaagctg gctgcaagaa ctctctctgg aagacattca catcctctta
351 g

L61 NUMBER 54 OF 52 CAPLUS COPYRIGHT 2005 ACS on STN.

Full Text

AT 1983-03821 CAPLUS

DN 89733821

TI Rat prostatic steroid binding protein: DNA sequence and transcript maps of the two C3 genes

AB Ewston, M. G.; Parker, M. G.

CS Inst. Cancer Res. Fund, London, WC2A 3PX, UK

SO EMBO Journal (1983), 2(5), 769-74

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CODEN: EMJODG; ISSN: 0261-4189

DT Journal

LA English

AB In the rat, there are 2 nonallelic genes, C3(1) and C3(2), for the C3 polypeptide and prostatic steroid-binding protein. Both genes were cloned and sequenced. Only C3(1) is responsible for the prodn. of authentic C3. Although there is a marked difference in their transcriptional activity, the 2 genes share extensive DNA sequence homol., there being only 1 base difference from nucleotide -235 to within the 1st intron. Transcript mapping showed that there are 2 distinct C3 transcripts which share a unique 3' terminus but have 5' termini 38 bases apart, each preceded by a TATA box homol. An identical repetitive element is present just upstream of both genes. Both families of transcripts, which are produced in a ratio of 18:1, are coordinately related by testosterone.

IT 86728-83-2 86243-28-9

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

STN Columbus

RN 84789-32-2 CAPLUS
 CH DNA (rat prostatein subunit C3 cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaagctgg tgtttctatt cttgttggtc accatcccta tttgctgcta
 51 tgccagtggc tctggctgca gtattctaga tgaagttatt agaggtacaa
 101 ttaactcaac tgtgacttta catgactata tgaattagt taagccatat
 151 gtacaagatc attttactga aaaggctgtg aagcaattca agcagtgttt
 201 tctagatcag accgacaaga ctctggaaaa tgttggcgtg atgatggagg
 251 caatatttaa cagtgaagc tgtcaacagc catcctaa

RN 86243-28-9 CAPLUS
 CN DNA (rat prostatein subunit C3(2) gene coding region) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaagctgg tgtttctatt cttgttggtc accatcccca tttgctgcta
 51 tgccagtggc tctggctgca gtattctaga tgaagttatt agaggtacaa
 101 ttaattcaac tgtgacttta catgactata tgaattagt taagccatat
 151 gtacatgac attttactgc aaatgctgtg aagcaattca agcagtgttt
 201 tctagatcag accaacaaga ctgttgaaaa tgttggcgtg atgacggagg
 251 caatatttaa cagtgaagc tgtcaacagc catcctaa

L61 ANSWER 55 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

FULL TEXT

AN 86091-26-1 CAPLUS

DS 13 10701

TE Rat pre-prosomatostatin. Structure and processing by microsomal membranes

AD Goodwin, Richard H.; Aron, David C.; Roos, Bernard A.

CS Lab. Mol. Endocrinol., Massachusetts Gen. Hosp., Boston, MA, 02111, USA

SO Journal of Biological Chemistry (1983), 258(9), 5570-3

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CODEN: JBCHA3; ISSN: 0021-9258

DT Current

LA English

AB The complete sequence of rat preprosomatostatin [86091-26-1], deduced from the nucleotide sequence of cDNAs derived from a somatostatin-rich medullary thyroid carcinoma is presented. Rat preprosomatostatin contains 116 amino acids (12,737 daltons). Cell-free translations of medullary thyroid carcinoma mRNA with dog pancreas microsomal membranes were performed to identify the cleavage point of the leader region from preprosomatostatin. Partial microsequencing data indicates that the cleavage occurs between the glycine and alanine at positions 24 and 25 of preprosomatostatin. Thus, rat prosomatostatin [86089-95-4] contains 92 amino acids (10,388 daltons). Comparison of the amino acid sequences of the rat and human preprosomatostatins reveals only 4 amino acid substitutions. The high level of conservation between rodents and humans of the entire preprosomatostatin mol. further suggests the possibility of biological functions of the NH2-terminal portions of prosomatostatin.

IT 86089-95-4

REL: RPD (Properties)

(nucleotide sequence of)

RN 86089-46-2 CAPLUS

CH DNA (rat somatostatin cDNA) (9CI) (CA INDEX NAME)

STN Columbus

NTE doublestranded

SEQ 1 atgctgtcct gccgtctcca gtgcgcgctg gccgcgctct gcacgtcct
51 ggctttgggc ggtgtcaccg gggcgccctc ggaccccaga ctccgtcagt
101 ttctgcagaa gtctctggcg gctgccaccg ggaaacagga actggccaag
151 tacttcttgg cagaactgct gtctgagccc aaccagacag agaacgatgc
201 cctggagcct gaggatttgc cccaggcagc tgagcaggac gagatgaggc
251 tggagctgca gaggtctgcc aactcgaacc cagccatggc accccgggaa
301 cgcaaagctg gctgcaagaa cttcttcttg aagacattca catcctgtta
351 g

L61 ANSWER 56 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:102042 CAPLUS

DN 98:102042

TI Prostatic steroid-binding protein. Isolation and characterization of C3 genes

AU Parker, Malcolm G.; White, Roger; Hurst, Helen; Needham, Maurice; Tilly, Rita

CS Imp. Cancer Res. Fund, London, WC2A 3PX, UK

SC Journal of Biological Chemistry (1983), 258(1), 12-15

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CODEN: JECHA3; ISSN: 0021-9258

DT Journal

LA English

AB Prostatic steroid-binding protein, the expression of which is stimulated by androgens, consists of 2 subunits, 1 contg. the polypeptides C1 and C3, and the other contg. the polypeptides C2 and C3. C3 mRNA-specific cDNA clones were isolated, sequenced, and used to isolate and characterize genomic clones for 2 C3 genes. Both genes are 3.2 kilobases with identical exon/intron arrangements; this is similar to the organization of C1 and C2 genes, which suggests that they might have arisen by duplications of an ancestral gene. Homologous human genes were not detected.

PT 98700042-2

REL 987 (Properties); BIOL (Biological study)

REL 987 (Nucleotide sequence of)

IN 98700-32-2 CAPLUS

CN RNA (rat prostatein subunit C3 cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaagctgg ttttgcattt atgtttggc accatcccta ttgtcgtca
51 tgccagtggc tctgttgcga gtattctaga tgaagttatt agaggtacaa
101 ttaactcaac cctggcctta tatgactata tgaaattagt taagccatat
151 gtacaagatc atttactga aaaggctgtg aagcaattca agcagtgtt
201 cctagatcag accgacaga tcttggaata tgttggcgtg atgatggagg
251 caataattaa cagtgaaga ggtcaacaga catcctaa

L61 ANSWER 57 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:47849 CAPLUS

DN 98:47849

TI Alternative RNA processing in calcitonin gene expression generates mRNAs encoding different polypeptide products

AU Amara, Susan G.; Jonas, Vivian; Rosenfeld, Michael G.; Ong, Estelita S.;

STN Columbus

Evans, Ronald M.
CS Div. Endocrinol., Univ. California Sch. Med., San Diego, CA, 92093, USA
SO Nature (London, United Kingdom) (1982), 292(5871), 240-4

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CODEN: NATUAS; ISSN: 0028-0836

DT Journal

LA English

AB Alternative processing of RNA transcripts from the calcitonin gene resulted in the prodn. of distinct mRNAs encoding the hormone calcitonin [9007-12-9] or a predicted product referred to as calcitonin gene-related peptide (CGRP) [83652-28-2]. The calcitonin mRNA predominated in the thyroid whereas the CGRP-specific mRNA appeared to predominate in the hypothalamus. A model is proposed in which developmental regulation of RNA processing is used to increase the diversity of neuroendocrine gene expression.

IT 83667-67-8

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 83667-67-8 CAPLUS

CN DNA (rat hypothalamus preprocalcitonin gene-related peptide cDNA) (9CI)
(CA INDEX NAME)

NFB doublestranded

SEQ
1 atgggcttcc tgaagttctc ccctttcctg gttgtcagca tcttgctcct
51 gtaccaggca tgcggcctcc aggcagtcc tttagaggta accttagaaa
101 gcagcccagg catggccact ctcaagtgaag aagaagctcg cctactggct
151 gcactggtgc agaactatat gcagatgaaa gtcaggagagc tggagcagga
201 ggaggaaacag gagcctgagc gctctagagt cactgcccag aagagatcct
251 gcaacactgc cactgctg acccatcggc tggcaggctt gctgagcagg
301 cccggaggty tggtagaggatcaacttctg cccaccaatg tgggctctga
351 agcctctgcc cgcgcacgca gggaccttca ggcttga

ANSWER 58 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

AN 1982-586654 CAPLUS

BN 97-586654

TI Human somatostatin I: sequence of the cDNA

AB Shen, Lu Ping; Pictet, Raymond L.; Rutter, William J.

SO Dep. Biochem. Biophys., Univ. California, San Francisco, CA, 94143, USA
Proceedings of the National Academy of Sciences of the United States of America (1982), 79(15), 4575-9

====
CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB RNA has been isolated from a human pancreatic somatostatinoma and used to prepare a cDNA library. After prescreening, clones contg. somatostatin I sequences were identified by hybridization with an anglerfish somatostatin I-cloned cDNA probe. From the nucleotide sequence of 2 of these clones, an essentially full-length mRNA sequence, including the preprosomatostatin-coding region, 105 nucleotides from the 5' untranslated region and the complete 150-nucleotide 3' untranslated region, have been deduced. The coding region predicts a 116-amino acid precursor protein [83271-75-4] (Mr, 12,727) that contains human somatostatin I [40958-31-4] and -28 [75306-06-8] at its COOH terminus. The predicted amino acid sequence of human somatostatin-28 is identical to that of somatostatin-28 isolated from the porcine and ovine species. A comparison of the amino acid sequences of human and anglerfish preprosomatostatin I indicated that

STN Columbus

the COOH-terminal region encoding somatostatin-14 and the adjacent 6 amino acids are highly conserved, whereas the remainder of the mol., including the signal peptide regions, is more divergent. However, many of the amino acid differences found in the pro region of the human and anglerfish proteins are conservative changes. This suggests that the propeptides have a similar secondary structure, which in turn may imply a biol. function for this region of the mol.

IT 83270-98-8

RL: PRF (Properties)

(nucleotide sequence of)

RN 83270-98-8 CAPLUS

CN DNA (human preprosomatostatin I cDNA) (9CI) (CA INDEX NAME)

```

SEQ      1 atgctgtcct gccgcctcca gtgcgcgctg gctgcgctgt ccacgtcct
      51 ggccctgggc tgtgtcaccg gcgtccctc ggaccccaga ctccgtcagt
     101 ttctgcagaa gtccttggt gctgccgagg ggaagcagga actggccaag
     151 cacttcttgg cagagctgct gtctgaacc aaccagacgg agaagatgac
     201 cctggaacct gaagatctgt cccaggctgc tgagcaggat gaaatgaggg
     251 ttgagctgca gagatctgct aactcaaacc cggctatggc accccgagaa
     301 cgcaaagctg gctgcaagaa tttcttctgg aagactttca catcctgtta
     351 g

```

LBI NUMBER 59 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Name

AC 1982-401509 CAPLUS

DT 27-1982

TF Somatostatin or somatostatin precursors

IN Hobbs, Peter; Crawford, Robert; Pictet, Raymond L.; Rutter, William J.

PA University of California, Berkeley, USA

SO Ann. Rev. Appl., 50 pp.

CO 13. INF:XDW

IT

LA English

CONCISE

PROJECT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 46559	A1	19820303	EP 1981-303825	19810821
EP 46559	B1	19841024		
EP, AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
ZA 3105571	A	19820825	ZA 1981-5671	19810817
IL 63679	A1	19850630	IL 1981-63629	19810820
FI 8144593	A	19820226	FI 1981-2593	19810821
AT 3884	E	19841115	AT 1981-303825	19810821
DK 3162727	A	19820226	DK 1981-3727	19810824
AU 3144178	A1	19820304	AU 1981-74478	19810824
JP 547147	B2	19860206		
JP 57776455	A2	19820806	JP 1981-133229	19810824
ES 304319	A1	19830101	ES 1981-504929	19810824
HU 12739	C	19840228	HU 1981-2454	19810824
DD 202451	A5	19830914	DD 1981-232787	19810825
ES 514528	A1	19830416	ES 1982-514528	19820729
FR 1980-181046	A	19800825		
EP 1981-303825	A	19810821		

AF cDNA sequences for somatostatin and its precursors are cloned. Thus, poly(A)-contg. RNA was isolated from Brockmann bodies of the anglerfish (*Lophius americanus*) and used as a template to synthesize cDNA, which was subsequently provided with dC tails. Plasmid pBR322 was cleaved by restriction endonuclease PstI and provided with dG tails. Equimolar amts.

STN Columbus

of dG-tailed cDNA and dG-tailed pBR322 were annealed and used to transform *Escherichia coli* X1776, and tetracycline-resistant transformants were selected. Transformants contg. anglerfish sequences were identified by colony hybridization, with a 32P-labeled cDNA synthesized from anglerfish Brockmann body poly(A)-contg. RNA as probe. Purified insert cDNAs from 2 of the colonies were sequenced. One recombinant plasmid (pLaS1) contained DNA coding for preprosomatostatin [75037-28-4]-1; another (pLaS2) coded for somatostatin [51110-01-1]-2. DNA sequences coding for prosomatostatin [74315-46-1]-1, preprosomatostatin-2, and prosomatostatin-2 were also cloned.

IT 77000-19-2

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 77000-19-2 CAPLUS

CN DNA (*Lophius americanus* preprosomatostatin II cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgcagtgta tccgttgctc cgccatcttg gctctcctgg cgttggttct
51 gtgcggccca agtgtttcct cccagctcga cagagagcag agcgacaacc
101 aggacctgga cctggagctg cgtcagcact ggctgctgga gagagcccg
151 agcgccggac tctgtccca ggagtggagt aaacgggcgg tggaggagct
201 gctggctcag atgtctctgc cagaggccac gttccagcgg gaggcggagg
251 acgctcccat ggcaacagaa ggacggatga acctagagcg gtccgtggac
301 tctaccaaca acctaccccc tctgtagcgt aaagctggct gtaagaactt
351 ctattggaag gggttcacat cctgt

ESA ANSWER 60 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1982-194232 CAPLUS

DN 96-194132

TI Overlap between ampC and fcd operons on the *Escherichia coli* chromosome

AU O. Andersson, Thomas Gaurin, Bengt Aake

CS Dep. Microbiol., Univ. Umeaa, Umeaa, S-901 87, Swed.

SO Proceedings of the National Academy of Sciences of the United States of America (1982), 79(4), 1111-15

====

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB The promoter for the *E. coli* ampC β -lactamase [9073-60-3] gene is located within the last gene of the fumarate reductase [9076-99-7] (frd) operon. Evidently, the ampC attenuator serves as the terminator for transcription of this preceding operon. The nucleotide sequence was detd. for 2 proteins that are encoded by a DNA segment preceding the ampC gene. The 2 proteins consisted of 131 and 119 triplets and had mol. wts. of 15,000 and 13,100, resp. The 12 COOH-terminal amino acids of the 13,100-dalton protein overlapped the ampC promoter. Accordingly, a 3'-G insertion in the promoter gave both increased transcription of ampC and a frameshift in this overlapping gene, resulting in readthrough proteins. Thus, a type of very compact genetic organization of operons in prokaryotes is described.

IT 31669-81-0

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 31669-81-0 CAPLUS

CN DNA (*Escherichia coli* frd operon 13.1-kilodalton protein gene) (9CI) (CA INDEX NAME)

STN Columbus

NTE Doublestranded

```

SEQ      1 atgattaatc caaatccaaa gcgttctgac gaaccggtat tctggggcct
        51 cttcggggcc gggtgtatgt ggagcgcgat cattgcgccg gtgatgatcc
       101 tgctgggtggg tattctgctg ccactggggg tgttccggg tgatgcgctg
       151 agctacgagc gcgttctggt gtgcgcgag agcttcattg gtcgcgtatt
       201 cctgttctctg atgatcgttc tgccgctgtg gtgtggttta caccgtatgc
       251 accacgcgat gcacgatctg aaaatccacg tacctgcggg caaatgggtt
       301 ttctacggtc tggtgtctat cctgacagtt gtcacgctga ttggtgtcgt
       351 tacaatctaa
  
```

L61 ANSWER 61 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1982:46833 CAPLUS

DN 96:46833

TI Regulation of the S10 ribosomal protein operon in E. coli: nucleotide sequence at the start of the operon

AU Olin's, Peter O.; Nomura, Masayasu

CS Inst. Enzyme Res., Univ. Wisconsin, Madison, WI, 53706, USA

SO Cell (Cambridge, MA, United States) (1981), 26(2, Pt. 2), 205-11

====

CODEN: CELLB5; ISSN: 0092-8674

DT Journal

LA English

AB The DNA sequence of a 1250-base-pair segment of the Escherichia coli chromosome that carries the promoter for the S10 ribosomal protein operon, the S10 gene, and part of the L3 gene was detd. A DNA fragment carrying the putative S10 promoter was cloned into the plasmid mini-Col E1, which contains a transcription termination signal close to the single HindII site. Cells harboring the hybrid plasma produced a relatively stable hybrid mRNA with the expected sequence, demonstrating that the promoter functions in vivo. Comparison of the mRNA sequence around the start of the S10-coding region, the presumed target site for L4 repressor protein, with the known binding site for L4 on 23 S rRNA revealed the presence of sequence homologies. This supports the model of the translational feedback regulation of the S10 operon by L4.

JT 80451-23-6

FT PRO (Properties); BTOL (Biological Study)
(nucleotide sequence of)

DN 80451-23-6 CAPLUS

CM PRO (Escherichia coli ribosome protein S 10 gene) (SCI) (CA INDEX NAME)

```

SEQ      1 atgcagaacc aaagaatccg taccgcctg aaagcgttctg atcattcgtct
        51 atcgcataaa gcaacggcgg aaacggtcga gactgccaaag cgcactgggtg
       101 cgcaggtccg tggtcggatc ccgctgccga caacgaaaga gcgttccact
       151 ttctctgata cccgcacagt caacaaagac gcgcgcgata agtacgaaat
       201 ccgtactcac ttgcgtctgg ttgacatcgt cgagcgaacc gagaaaaccg
       251 ttgatgctct gatcgctctg gatctggctg ccggtctaga cgtgcagatc
       301 agcctggggt aa
  
```

L61 ANSWER 62 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:134404 CAPLUS

DN 94:134404

TI Cloning and sequence analysis of cDNAs encoding two distinct somatostatin

STN Columbus

precursors found in the endocrine pancreas of anglerfish
 AU Hcbart, Peter; Crawford, Robert; Shen, Lu Ping; Pictet, Raymond; Rutter, William J.
 CS Dep. Biochem. Biophys., Univ. California, San Francisco, CA, 94143, USA
 SO Nature (London, United Kingdom) (1980), 288(5787), 137-41

====

CODEN: NATUAS; ISSN: 0028-0836
 DT Journal
 LA English
 AB Complementary DNAs for 2 distinct anglerfish (*Lophius americanus*) somatostatin peptides (I and II) were cloned in bacterial plasmids and sequenced. The nucleotide sequence for somatostatin I encoded a large precursor peptide (mol. wt. 13,300) in which the somatostatin hormone was at the carboxyl terminus. The predicted 14-amino acid sequence for anglerfish somatostatin I was the same as mammalian somatostatin. Somatostatin II was also formed as part of a larger precursor (mol. wt. 14,100) with the presumptive somatostatin hormone also at the carboxyl terminus. The 14-amino acid sequence of somatostatin II differed from somatostatin I at 2 internal residues (tyrosine in place of phenylalanine 7 and glycine in place of threonine 10). The 2 different somatostatins may have distinct biol. activities. Homologies in the amino acid sequences of the 2 peptides outside the somatostatin moiety suggested that other regions of the mols. may have biol. functions.

IT 77000-19-2

RL: ERP (Properties)
 (nucleotide sequence of)

RN 77000-19-2 CAPLUS

CN DNA (*Lophius americanus* preprosomatostatin II cDNA) (9CI) (CA INDEX NAME)

NEZ Doublestranded.

SEQ
 1 atcagtgta tccgttgcc agccatcttg gcctcctgg cgttggttct
 2 tgcggccca agtggttctt cccagctcga cagagagcag agcgacaacc
 3 tggacctgga cctggagctg cgtcagcact ggctgctgga gagagccggg
 4 tgggcccggg tctgttccca ggagtggagt aaacggggcg tggaggagct
 5 gctggctcag atgtctctgc cagaggccac gttccagcgg gaggcggagg
 6 acggtcccat ggcaacagaa ggacygatga acctagagcg gtccgtggac
 7 tctaccaaca acctacccc tctgagcgt aaagctggct gtaagaactt
 8 tctattggaag gggttcactt cctgt

=> d has

(PAGE 'HOME' ENTERED AT 15:37:06 ON 29 APR 2005)

(PAGE 'REGISTRY' ENTERED AT 15:37:19 ON 29 APR 2005)

L1 0 S CTGGCTGC/SQEN
 L2 0 S CTGGCTGCCT/SQEN
 L3 0 S CTGGCTGCCTGG/SQEN
 L4 3015 S CTGGCTGCCTGG/SQSN
 L5 190 S L4 AND SQL<=375

(PAGE 'CAPLUS' ENTERED AT 15:41:43 ON 29 APR 2005)

L6 0 S L5 AND PY<1990
 L7 1010 S L4
 L8 3 S L7 AND PY<1990
 L9 106 S L5
 L10 0 S L5 AND PY<1991
 L11 0 S L9 AND PY<1991

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FILE 'REGISTRY' ENTERED AT 15:45:39 ON 29 APR 2005
 L12 0 S TCACCAGCCC/SQEN
 L13 78505 S TCACCAGCCC/SQSN

FILE 'CAPLUS' ENTERED AT 15:46:49 ON 29 APR 2005
 L14 7141 S L13
 L15 64 S L14 AND PY<1990

FILE 'REGISTRY' ENTERED AT 15:48:16 ON 29 APR 2005
 L16 5749 S L13 AND SQL<400

FILE 'CAPLUS' ENTERED AT 15:48:46 ON 29 APR 2005
 L17 1318 S L16
 L18 2 S L17 AND PY<1990

FILE 'REGISTRY' ENTERED AT 15:50:45 ON 29 APR 2005
 L19 0 S TTCATTGACG/SQEN
 L20 21130 S TTCATTGACG/SQSN
 L21 0 S TTCATTGATG/SQEN
 L22 94859 S TTCATTGATG/SQSN
 L23 6265 S L22 AND SQL<400

FILE 'CAPLUS' ENTERED AT 15:53:46 ON 29 APR 2005
 L24 1521 S L23
 L25 1 S L24 AND PY<1990

FILE 'REGISTRY' ENTERED AT 15:54:22 ON 29 APR 2005
 L26 0 S CATCAGTGGG/SQEN
 L27 58750 S CATCAGTGGG/SQSN
 L28 4611 S L27 AND SQL<400

FILE 'CAPLUS' ENTERED AT 15:55:37 ON 29 APR 2005
 L29 1211 S L28
 L30 3 S L29 AND PY<1990

FILE 'REGISTRY' ENTERED AT 15:58:08 ON 29 APR 2005
 L31 0 S TGCTGTCCAG/SQEN
 L32 82727 S TGCTGTCCAG/SQSN
 L33 6562 S L32 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:00:16 ON 29 APR 2005
 L34 1650 S L33
 L35 1 S L34 AND PY<1990

FILE 'REGISTRY' ENTERED AT 16:01:17 ON 29 APR 2005
 L36 0 S GTTCGATCAG/SQEN
 L37 23723 S GTTCGATCAG/SQSN
 L38 1949 S L37 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:03:02 ON 29 APR 2005
 L39 575 S L38
 L40 2 S L39 AND PY<1990

FILE 'REGISTRY' ENTERED AT 16:04:42 ON 29 APR 2005
 L41 0 S GGCCTCCTGC/SQEN
 L42 96510 S GGCCTCCTGC/SQSN
 L43 8374 S L42 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:06:32 ON 29 APR 2005
 L44 1768 S L43
 L45 2 S L44 AND PY<1990

STN Columbus

FILE 'REGISTRY' ENTERED AT 16:09:19 ON 29 APR 2005

L46 0 S AGACCGCGTC/SQEN
L47 13729 S AGACCGCGTC/SQSN
L48 1216 S L47 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:11:18 ON 29 APR 2005

L49 278 S L48
L50 1 S L49 AND PY<1990

FILE 'REGISTRY' ENTERED AT 16:12:10 ON 29 APR 2005

L51 0 S ACAGGGAAGT/SQEN
L52 63875 S ACAGGGAAGT/SQSN
L53 4067 S L52 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:13:55 ON 29 APR 2005

L54 1146 S L53
L55 1 S L54 AND PY<1990
S CTGGCTGC/SQEN

FILE 'REGISTRY' ENTERED AT 16:15:32 ON 29 APR 2005

L56 0 S CTGGCTGC/SQEN

FILE 'CAPLUS' ENTERED AT 16:15:33 ON 29 APR 2005

L57 0 S L56

FILE 'REGISTRY' ENTERED AT 16:16:01 ON 29 APR 2005

L58 106010 S CTGGCTGC/SQSN
L59 111581 S L58 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:17:28 ON 29 APR 2005

L60 6250 S L59
L61 62 S L60 AND PY<1990

=> log y

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

TOTAL ESTIMATED COST

491.29

1097.57

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE

TOTAL

ENTRY

SESSION

CA SUBSCRIBER PRICE

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-57.67

STN INTERNATIONAL LOGOFF AT 16:36:52 ON 29 APR 2005

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NEWS 1 Web Page URLs for STN Seminar Schedule - N. America
 NEWS 2 "Ask CAS" for self-help around the clock
 NEWS 3 FEB 25 CA/CAPLUS - Russian Agency for Patents and Trademarks
 (ROSPATENT) added to list of core patent offices covered
 NEWS 4 FEB 28 PATDPAFULL - New display fields provide for legal status
 data from INPADOCC
 NEWS 5 FEB 28 BABS - Current-awareness alerts (SDIs) available
 NEWS 6 FEB 28 MEDLINE/LMEDLINE reloaded
 NEWS 7 MAR 02 GBFULL: New full-text patent database on STN
 NEWS 8 MAR 03 REGISTRY/ZREGISTRY - Sequence annotations enhanced
 NEWS 9 MAR 03 MEDLINE file segment of TOXCENTER reloaded
 NEWS 10 MAR 22 KOREAPAT now updated monthly; patent information enhanced
 NEWS 11 MAR 22 Original IDE display format returns to REGISTRY/ZREGISTRY
 NEWS 12 MAR 22 PATDPASPC - New patent database available
 NEWS 13 MAR 22 REGISTRY/ZREGISTRY enhanced with experimental property tags
 NEWS 14 APR 04 EPFULL enhanced with additional patent information and new
 fields
 NEWS 15 APR 04 EMBASE - Database reloaded and enhanced
 NEWS 16 APR 18 New CAS Information Use Policies available online
 NEWS 17 APR 25 Patent searching, including current-awareness alerts (SDIs),
 based on application date in CA/CAPLUS and USPATFULL/USPAT2
 may be affected by a change in filing date for U.S.
 applications.
 NEWS 18 APR 28 Improved searching of U.S. Patent Classifications for
 U.S. patent records in CA/CAPLUS
 NEWS EXPRESS JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT
 MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
 AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005
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=> file registry		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.21

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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
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<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s tgcttacat/sqen
      0 TGCTTACAT/SQEN
107453 SQL=9
L1      0 TGCTTACAT/SQEN
      (TGCTTACAT/SQEN AND SQL=9)
```

```
=> s tgcttacat/sqsn
L2      201666 TGCTTACAT/SQSN
```

```
=> s 12 and SQL<400
      22713436 SQL<400
L3      14623 L2 AND SQL<400
```

=> file registry	SINCE FILE	TOTAL
COST IN U.S. DOLLARS	ENTRY	SESSION
FULL ESTIMATED COST	39.81	40.02

FILE 'REGISTRY' ENTERED AT 16:57:30 ON 29 APR 2005
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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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STN Columbus

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

Please note that search-term pricing does apply when conducting SmartSELECT searches.

```
*****
*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*
*****
```

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s l3
      22713436 SQL<400
L4      14623 L2 AND SQL<400
```

```
=> s l4 and PY<1987
'1987' NOT A VALID FIELD CODE
      0 PY<1987
L5      0 L4 AND PY<1987
```

	SINCE FILE	TOTAL
COST IN U.S. DOLLARS	ENTRY	SESSION
FULL ESTIMATED COST	5.03	45.05

FILE 'CAPLUS' ENTERED AT 16:58:18 ON 29 APR 2005
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FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

```
=> s l3
L6      2668 L3
```

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=> s 16 and PY<1987
11536051 PY<1987
L7 4 L6 AND PY<1987

=> d bib ab hitseq 1-4

L7 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:536266 CAPLUS
DN 103:136266
TI Cotranscription of the large and small subunit genes of ribulose
1,5-bisphosphate carboxylase/oxygenase in *Cyanophora paradoxa*
AU Starnes, S. M.; Lambert, D. H.; Maxwell, E. S.; Stevens, S. E., Jr.;
Porter, R. D.; Shively, J. M.
CS Dep. Biol. Sci., Clemson Univ., Clemson, SC, 29631, USA
SO FEMS Microbiology Letters (1985), 28(2), 165-9
CODEN: FMLED7; ISSN: 0378-1097
DT Journal
LA English
AB The region of the cyanelle genome of *C. paradoxa* which codes for
ribulose-1,5-diphosphate carboxylase/oxygenase (I) [9027-23-0] was cloned
and partially characterized. The large subunit gene (*rbcL*) is located
adjacent to, and upstream from the small subunit gene (*rbcS*). The *rbcS*,
contg. 318 nucleotides, codes for a polypeptide that exhibits greater
homol. to small subunits of cyanobacteria than to those of angiosperms.
Immediately downstream from the *rbcS* termination codon is an apparent
transcription termination site consisting of an inverted repeat followed
by a T cluster. The spacer region sepg. *rbcL* and *rbcS* is 105 nucleotides
in length and lacks an obvious RNA polymerase promoter sequence suggesting
that the genes are cotranscribed. Northern blot anal. has confirmed the
contranscription of both genes as a single transcript of ~2500
nucleotides.

IT 98443-94-8

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 98443-94-8 CAPLUS

CN DNA (*Cyanophora paradoxa* cyanelle gene *rbcS*) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgcaactta gagtagaacg taagttcgaa actttttctt atttaccacc
51 attaaacgac caacagattg cgcgtcaatt acaatacgca ctttccaatg
101 gttatagccc agcaatcgaa ttcagtttta caggtaaaagc tgaagactta
151 gtatggactt tatggaaatt acctttattt ggtgcacaat ctctgaaga
201 agtacttagc gaaattcaag cttgtaaaca acagttccct aatgcttaca
251 ttcgtgttgt agcatttgac tctatcagac aagttcaaac tttaatgttc
301 ttagtttaca aaccattata g

L7 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:417579 CAPLUS

DN 103:17579

TI Phage P22 lysis genes: nucleotide sequences and functional relationships
with T4 and λ genes

AU Rennell, Dale; Poteete, Anthony R.

CS Med. Sch., Univ. Massachusetts, Worcester, MA, 01605, USA

SO Virology (1985), 143(1), 280-9

====

CODEN: VIRLAX; ISSN: 0042-6822

STN Columbus

DT Journal
 LA English
 AB Wild-type and amber mutant alleles of the lysis genes of phage P22 were cloned and sequenced. Gene 13 encodes an 11,520-dalton basic hydrophobic protein that has 89% amino acid homol. to λ S protein. Gene 19 encodes a protein that has a small degree of amino acid homol. with phage T4 lysozyme, but no homol. could be detected to λ R or RZ proteins. The protein product of gene 19 was purified; its N-terminal amino acid sequence is as predicted by the DNA sequence. It starts with a single N-terminal methionine residue and is a basic protein with a mol. wt. of 15,968. Plasmids expressing P22 gene 19, λ genes R and RZ, and T4 gene e were constructed. All of these plasmids were able to complement both λ R- and P22 19-.

IT 97047-61-5 97047-67-1

RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)

RN 97047-61-5 CAPLUS

CN DNA (enterobacteria phage P22 gene 13) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaaaaaga tgccagaaaa acatgatctg ttaaccgcca tgatggcggc
 51 aaaggaacag ggcacgagg caatcctcgc gtttgcaatg gcgtaccttc
 101 gcggtcggta taatggcggt gcgtttaaga aaacactaat agacgcaacg
 151 atgtgcgcca ttatgcctg gttcattcgt gaccttttag tcttcgccgg
 201 actgagtagc aatcttgctt acatagcgag tgtgtttatc ggctacatcg
 251 gcacagactc gattgggttcg ctaatcaaac gcttcgctgc taaaaaagcc
 301 ggagtcgatg atgcaaatca gcagtaa

RN 97047-67-1 CAPLUS

CN DNA (enterobacteria phage P22 gene 13 mutant 13-h21) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaaaaaga tgccagaaaa acatgatctg ttaaccgcca tgatggcggc
 51 aaaggaacag ggcacgagg caatcctcgc gtttgcaatg gcgtaccttc
 101 gcggtcggta taatggcggt gcgtttaaga aaacactaat agacgcaacg
 151 atgtgcgcca ttatgcctg tttcattcgt gaccttttag tcttcgccgg
 201 actgagtagc aatcttgctt acatagcgag tgtgtttatc ggctacatcg
 251 gcacagactc gattgggttcg ctaatcaaac gcttcgctgc taaaaaagcc
 301 ggagtcgatg atgcaaatca gcagtaa

L7 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:564673 CAPLUS

DN 101:164673

TI Tau, sigma, and delta. A family of repeated elements in yeast

AU Genbauffe, Francis S.; Chisholm, George E.; Cooper, Terrance G.

CS Dep. Biol. Sci., Univ. Pittsburgh, Pittsburgh, PA, 15260, USA

SO Journal of Biological Chemistry (1984), 259(16), 10518-25

====

CODEN: JBCHA3; ISSN: 0021-9258

DT Journal

LA English

AB The isolation and structure of a new repeated DNA element, tau, is reported. This element, from *Saccharomyces cerevisiae*, is 371 base pairs

STN Columbus

(bp) long and is flanked on either end by the same invertedly repeated sequence found at the ends of some Ty and sigma elements in yeast, copia elements in Drosophila, and spleen necrosis virus. The tau inverted repeats are themselves flanked by a 5-bp directly repeated genomic sequence that is present only once in a cognate tau- allele. These structural characteristics, the presence of multiple copies of tau in the genome, and the isolation of tau+ and tau- allelic pairs suggest that tau may be capable of transposition either alone or in assocn. with some larger element. Detailed sequence anal. of the tau, sigma, and delta elements revealed that all 3 contain significant regions of homol., suggesting that they are probably members of a single family derived from a common progenitor.

IT 91756-05-7 92584-26-4

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 91756-05-7 CAPLUS

CN DNA (Saccharomyces cerevisiae clone pFG26 tau element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 tgttggaaacg agagtaatta atagtgcacat gagttgctat ggtaacaatt
51 caatgcttac atcgatatatt aatgtacaac tcgtatacgt ttaagtgtga
101 ttgcgcctat tgcagaagga atgttaaacy agaagctcag acaatactga
151 agctgtgtta aagacctatt agttgaacat gttatggtag gtacatatat
201 gaggaatatg agtcgtcaca tcaatgtata gtaactaccg gaatcactat
251 tatattgggtc atgattaata tgaccaatcg gcgtgtgttt tatataacctc
301 tcttatttag tataagaaga tcagtaatta tttcttcatt aatactaatt
351 ttttaacctct aattatcaac a

RN 92584-26-4 CAPLUS

CN DNA (Saccharomyces cerevisiae clone pGC106 tau element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 tgttggaaacg agagtaatta atagtgcacat gagttgctat ggtaacaatc
51 taatgcttac atcgatatatt aatgtacacc tcgtatacgt ttaagtgtga
101 ttgcgcctat tgcagaagga atgttaaacy agaagctcag acaatactga
151 agctgtgtta aacacctatt agttgaacat gttatggtag gtacatatat
201 gaggaatatg agtcgtcaca tcaatgtata gtaactaccg gaatcactat
251 tatattgggtc atgattaata tgaccaatcg gcgtgtgttt tatataacctc
301 tcttatttag tataagaaga tcagtaatta tttcttcatt aatactattt
351 ttttaacctct aattatcaac a

L7 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:505082 CAPLUS

DN 101:105082

TI tau, A repeated DNA sequence in yeast

AU Chisholm, George E.; Genbauffe, Francis S.; Cooper, Terrance G.

CS Dep. Biol. Sci., Univ. Pittsburgh, Pittsburgh, PA, 15260, USA

SO Proceedings of the National Academy of Sciences of the United States of America (1984), 81(10), 2965-9

====

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

STN Columbus

LA English
 AB A 371-base-pair (bp) repeated DNA element, tau, was found in *Saccharomyces cerevisiae*. The ends of tau are composed of a 5-bp inverted repeat, similar in sequence to those reported for the Ty, sigma, copia, and spleen necrosis virus elements. These inverted repeats are flanked by 5-bp direct repeats of a target sequence that occurs only once in an allele that lacks the tau element. This overall structure is characteristic of transposable elements. Like sigma, tau elements were found (in both orientations) closely assocd. with tRNA genes (409 and 198 bp from the 5' end, resp.). It is noteworthy that 1 representative of tau was isolated in a concentric insertion of tau, delta, and sigma.

IT 91756-05-7

RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)

RN 91756-05-7 CAPLUS

CN DNA (*Saccharomyces cerevisiae* clone pFG26 tau element) (9CI) (CA INDEX NAME)

NTE doublestranded

```
SEQ      1 tgttggaacg agagtaatta atagtgcacat gagttgctat ggtaacaatt
          51 caatgcttac atcgtatatatt aatgtacaac tcgtatacgt ttaagtgtga
          101 ttgcgcctat tgcagaagga atgttaaacy agaagctcag acaatactga
          151 agctgtgtta aagacctatt agttgaacat gttatggtag gtacatatat
          201 gaggaatatg agtcgtcaca tcaatgtata gtaactaccg gaatcactat
          251 tatattggtc atgattaata tgaccaatcg gcgtgtgttt tatataacctc
          301 tcttatttag tataagaaga tcagtaatta tttcttcatt aatactaatt
          351 tttaacctct aattatcaac a
```

=> file stnguide

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	33.69	78.74
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-2.92	-2.92

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FILE CONTAINS CURRENT INFORMATION.
 LAST RELOADED: Apr 22, 2005 (20050422/UP).

=> file registry

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.30	79.04
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-2.92

FILE 'REGISTRY' ENTERED AT 17:03:34 ON 29 APR 2005
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STN Columbus

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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

Please note that search-term pricing does apply when conducting SmartSELECT searches.

*
* The CA roles and document type information have been removed from *
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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s cactcatat/sqen
      0 CACTCATAT/SQEN
107453 SQL=9
L8      0 CACTCATAT/SQEN
      (CACTCATAT/SQEN AND SQL=9)
```

```
=> s cactcatat/sqsn
L9      157456 CACTCATAT/SQSN
```

```
=> s l9 and SQL<400
      22713436 SQL<400
L10      9780 L9 AND SQL<400
```

=> file caplus		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	39.81	118.85
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	-2.92

FILE 'CAPLUS' ENTERED AT 17:04:45 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s l10

L11 2154 L10

=> s l11 and PY<1987

11536051 PY<1987

L12 1 L11 AND PY<1987

=> d bib ab hitseq

L12 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:29657 CAPLUS

DN 104:29657

TI Burkitt lymphoma cell line carrying a variant translocation creates new DNA at the breakpoint and violates the hierarchy of immunoglobulin gene rearrangement

AU Denny, Christopher T.; Hollis, Gregory F.; Magrath, Ian T.; Kirsch, Ilan R.

CS Navy Med. Oncol. Branch, Natl. Cancer Inst., Bethesda, MD, 20205, USA

SO Molecular and Cellular Biology (1985), 5(11), 3199-207

CODEN: MCEBD4; ISSN: 0270-7306

DT Journal

LA English

AB The Burkitt lymphoma cell line KK124, which contains a reciprocal t(8;22) translocation, rearranged in a region 3' to the c-myc proto-oncogene on chromosome 8 and 5' to the λ const. region on chromosome 22. The breakpoint was cloned and sequenced, revealing the c-myc and a portion of its 3' region abutted a complete λ variable gene that had undergone V-J recombination. Since this cell line expresses κ light chain, this λ rearrangement violates the previously proposed hierarchy of Ig gene rearrangement. A novel duplication of normal chromosome 8 sequences was also found at the breakpoint. The 1st exon of c-myc and its flanking sequence from the translocated allele was sequenced and compared with a normal counterpart. Extensive mutation was found within the 1st exon, in contrast to its 3'- and 5'-flanking regions. S1 nuclease anal. revealed that the translocated c-myc was expressed and that there was a promoter shift from P2 to P1. The detailed structural anal. of this cell line provides clues concerning mechanisms of chromosomal translocation and c-myc deregulation in Burkitt lymphomas.

IT 99752-03-1

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 99752-03-1 CAPLUS

CN DNA (human Burkitt's lymphoma KK124 immunoglobulin V λ gene) (9CI)
(CA INDEX NAME)

NTE doublestranded

STN Columbus

```

SEQ      1 tctgccctga ctcagcctgc ctccgtgtct gggctcctg gacagtcgat
          51 caccatctcc tgcattggaa tcaacagtga catttgcggt tgtaactatg
        101 tctccgggta ccaacagcac ccagccaaag cccccaaact catgatttat
        151 gaggtcagta atcgccctc agggttttct aatcgcttct ctggctccaa
        201 gtctgccaac acggcctccc tgaccatctc tgggctccag gctgaggacg
        251 aggctgatta ttactacact catatacaga caccagcact ctcgggtg
  
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=> file registry

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

11.64

130.49

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE

TOTAL

ENTRY

SESSION

CA SUBSCRIBER PRICE

-0.73

-3.65

FILE 'REGISTRY' ENTERED AT 17:07:46 ON 29 APR 2005

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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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```

*****
*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*
*****
  
```

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s gaaggtcct/sqen

0 GAAGGTCCT/SQEN

107453 SQL=9

L13

0 GAAGGTCCT/SQEN

(GAAGGTCCT/SQEN AND SQL=9)

=> s gaaggtcct/sqsn

STN Columbus

L14 193989 GAAGGTCCT/SQSN

=> s 114 and SQL<400

22713436 SQL<400

L15 16920 L14 AND SQL<400

=> file caplus

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

39.81

170.30

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE

TOTAL

ENTRY

SESSION

0.00

-3.65

CA SUBSCRIBER PRICE

FILE 'CAPLUS' ENTERED AT 17:08:58 ON 29 APR 2005

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FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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=> s 115

L16 2703 L15

=> s 116 and PY<1987

11536051 PY<1987

L17 4 L16 AND PY<1987

=> d bib ab hitseq 1-4

L17 ANSWER 1 OF 4 CAPLUS. COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:83077 CAPLUS

DN 104:83077

TI Genetic expression of somatostatin as hybrid polypeptide

IN Canosi, Umberto; De Fazio, Gabriele; Villa, Stefano; Donini, Silvia

PA Istituto Farmacologico Serson S.p.A., Italy

SO Eur. Pat. Appl., 21 pp.

CODEN: EPXXDW

DT Patent

LA English

FAN.CNT 1

PATENT NO.

KIND

DATE

APPLICATION NO.

DATE

STN Columbus

PI	EP 160190	A2	19851106	EP 1985-102891	19850313 <--
	EP 160190	A3	19870715		
	R: AT, CH, DE, FR, GB, LI, NL, SE				
	IL 74620	A1	19901223	IL 1985-74620	19850315
	ZA 8502035	A	19851127	ZA 1985-2035	19850319 <--
	DK 8501312	A	19851001	DK 1985-1312	19850322 <--
	AU 8540461	A1	19851031	AU 1985-40461	19850328 <--
	FI 8501288	A	19851001	FI 1985-1288	19850329 <--
	NO 8501308	A	19851001	NO 1985-1308	19850329 <--
	ES 541782	A1	19860401	ES 1985-541782	19850329 <--
	CA 1301676	A1	19920526	CA 1985-477979	19850329
	JP 61005788	A2	19860111	JP 1985-65088	19850330 <--
	US 5268278	A	19931207	US 1988-193202	19880509
	AU 8939547	A1	19891130	AU 1989-39547	19890811
	AU 611048	B2	19910530		
PRAI	IT 1984-47976	A	19840330		
	US 1985-717444	B1	19850329		

AB Recombinant plasmid vectors are described that contain the entire Trp regulatory system (promoter, operator, leader, and attenuator) and a synthetic gene that encodes somatostatin. Thus a plasmid, pSP3, was constructed that contained the Trp regulatory region, the 1st 323 codons of the TrpE gene, and a linker sequence. A synthetic gene for somatostatin was prep'd. and inserted into the linker region of pSP3 to yield pSP4. Plasmid pSP4 encoded a fusion protein comprised of 323 amino acids of the TrpE protein, 4 amino acids encoded by the linker region, and somatostatin. The somatostatin was released from the fusion protein by CNBr treatment. The yield was ~300 µg somatostatin/L of *Escherichia coli* culture. The yield was increased to 400 µg/L if indole was used instead of tryptophan to derepress the tryptophan operon.

IT 100438-83-3

RL: PRF (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 100438-83-3 CAPLUS

CN DNA, (sheep somatostatin[Met-1]-specifying) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 agcttacatg gccggttgca agaacttctt ctggaagacc ttcacctctt
51 gctag

1 gatcctagca agaggtgaag gtctccaga agaagttctt gcaaccggcc
51 atgta

L17 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:573361 CAPLUS

DN 100:173361

TI Cloning and expression of the 1.3 S biotin-containing subunit of transcarboxylase

AU Murtif, Vicki L.; Bahler, Chris R.; Samols, David

CS Dep. Biochem., Case Western Reserve Univ., Cleveland, OH, 44106, USA

SO Proceedings of the National Academy of Sciences of the United States of America (1985), 82(17), 5617-21

====

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB The gene coding for the 1.3 S biotin-contg. subunit of transcarboxylase (EC 2.1.3.1) [9029-86-1] from *Propionibacterium shermanii* was cloned.

STN Columbus

Transcarboxylase is a well-characterized enzyme composed of 30 polypeptides of 3 different types; 12 1.3 S biotinyl subunits, 6 5 S dimeric outer subunits, and 1 12 S hexameric central subunit. In propionic acid ferment., the enzyme catalyzes the transfer of a carboxyl group from methylmalonyl-CoA to pyruvate in 2 partial reactions. The 1.3 S subunit binds the outer and central subunits of the enzyme together, and its biotin serves as carboxyl carrier between subsites on the central and outer subunits where each partial reaction occurs. The cloned gene was expressed in *Escherichia coli*, and the 1.3 S subunit accumulates to 7% of total cellular protein. The foreign protein is recognized and biotinylated by biotin holoenzyme synthetase of *E. coli*. The identifications of the gene and its product were confirmed by 4 independent approaches; DNA sequence anal., immunopptn., incorporation of labeled biotin, and measurement of enzymic activity in the 1st partial reaction.

IT 98824-75-0

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 98824-75-0 CAPLUS

CN DNA (Propionibacterium shermanii methylmalonyl coenzyme A carboxyltransferase biotinyl subunit gene) (9CI) (CA INDEX NAME)

SEQ 1 atgaaactga aggtaacagt caacggcact gcgtatgacg ttgacgttga
51 cgtcgacaag tcacacgaaa acccgatggg caccatcctg ttcggcggcg
101 gcaccggcgg cgcgccggca ccgcgcgcag caggtggcgc aggcgcgggt
151 aaggccggag agggcgagat tcccgctccg ctggccggca ccgtctccaa
201 gatcctcgtg aaggagggtg acacgggtcaa ggctggtcag accgtgctcg
251 ttctcgaggc catgaagatg gagaccgaga tcaacgtcc caccgacggc
301 aaggtcgaga aggtccttgt caaggagcgt gacgccgtgc agggcggtca
351 gggtctcatc aagatcgggt ga

I17 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:90720 CAPLUS

DN 102:90720

TI Molecular cloning and nucleotide sequence of a variant wheat histone H4 gene

AV Tabata, Tetsuya; Iwabuchi, Masaki

CS Fac. Sci., Hokkaido Univ., Sapporo, 060, Japan

SO Gene (1984), 31(1-3), 285-9

====

CODEN: GENED6; ISSN: 0378-1119

DT Journal

LA English

AB To det. whether there is structural variation among histone H4 genes in wheat, one (TH091) of the H4 genes that had been cloned from a wheat genomic DNA library was sequenced and compared with another H4 gene (TH011) described previously. There are 17 nucleotide replacements in the protein-coding region of 2 H4 genes, causing only 1 amino acid substitution: a glycine at position 4 (from the N.terminus) in TH011 was replaced by an aspartic acid in TH091. S1 mapping, using total nuclear RNA from germinated seeds, indicated that the H4 gene was transcribed in vivo.

IT 94895-12-2

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 94895-12-2 CAPLUS

CN DNA (wheat clone pTH091 histone H 4 gene) (9CI) (CA INDEX NAME)

STN Columbus

NTE doublestranded

```
SEQ      1 atgtctgggc gcgacaaggg cggcaagggg ctgggcaagg gcggcgccaa
          51 gcggcaccgg aaggtcctcc gcgacaacat ccagggcatc accaagccgg
          101 cgatccggag gctggccagg aggggcggcg tgaagcgcat ctccggcctc
          151 atctacgagg agaccgcggg cgtcctcaag atcttctcgc agaacgtcat
          201 ccgcgacgcc gtcacctaca ccgagcacgc ccgccgcaaa accgtcaccg
          251 ccatggacgt cgtctacgcg ctcaagcgcc agggccgcac cctctacggc
          301 ttcggaggct ag
```

L17 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:607278 CAPLUS

DN 99:207278

TI The structural organization and DNA sequence of a wheat histone H4 gene

AU Tabata, Tetsuya; Sasaki, Kimiko; Iwabuchi, Masaki

CS Fac. Sci., Hokkaido Univ., Sapporo, 060, Japan

SO Nucleic Acids Research (1983), 11(17), 5865-75

====

CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB Wheat histone H4 genes were cloned from a Charon 4 wheat genomic DNA library using sea urchin histone H4 DNA as a probe. DNA sequence anal. of a cloned gene showed that the deduced amino acid sequence of wheat histone H4 protein was identical to that of pea. The 5' end of wheat histone H4 mRNA was mapped on the cloned gene by the S1 procedure. Southern blot anal. of the genomic DNA indicated that histone H4 genes were reiterated 100-125 times/hexaploid wheat genome.

IT 87935-36-4

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 87935-36-4 CAPLUS

CN DNA (wheat clone pTH011 histone H4 gene) (9CI) (CA INDEX NAME)

NTE doublestranded

```
SEQ      1 atgtccgggc gcggcaaggg aggcaagggc ctaggcaagg gcggcgccaa
          51 gcgcccaccgg aaggtcctcc gcgataacat ccagggcatc accaagccgg
          101 cgatccggcg gctggcgcgg cggggcgggc tgaagcgcat ctccgggctc
          151 atctacgagg agaccgcggg cgtgctcaag atcttctcgc agaacgtcat
          201 ccgcgatgcc gtcacctaca ccgagcacgc ccgccgcaag accgtcaccg
          251 ccatggacgt cgtctacgcg ctcaagcgcc agggccgcac ctctacggct
          301 tcggcggtta a
```

=> file registry

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

34.59

204.89

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE

TOTAL

ENTRY

SESSION

CA SUBSCRIBER PRICE

-2.92

-6.57

FILE 'REGISTRY' ENTERED AT 17:12:32 ON 29 APR 2005

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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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*
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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s gggagtacg/sqen
      0 GGGAGTACG/SQEN
107453 SQL=9
L18   0 GGGAGTACG/SQEN
      (GGGAGTACG/SQEN AND SQL=9)
```

```
=> s gggagtacg/sqsn
L19   116522 GGGAGTACG/SQSN
```

```
=> s l19 and SQL<400
      22713436 SQL<400
L20   5701 L19 AND SQL<400
```

=> file caplus		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	39.81	244.70
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	-6.57

FILE 'CAPLUS' ENTERED AT 17:13:47 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s l20

L21 1154 L20

=> s l21 and PY<1987

11536051 PY<1987

L22 0 L21 AND PY<1987

=> s l21 and PY<1988

12016813 PY<1988

L23 0 L21 AND PY<1988

=> file registry

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

4.23

248.93

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE

TOTAL

ENTRY

SESSION

CA SUBSCRIBER PRICE

0.00

-6.57

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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*
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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s ggtatttga/sqen
      0 GGTATTTGA/SQEN
      107453 SQL=9
L24      0 GGTATTTGA/SQEN
          (GGTATTTGA/SQEN AND SQL=9)
```

```
=> s ggtatttga/sqsn
L25      182237 GGTATTTGA/SQSN
```

```
=> s 125 and SQL<400
      22713436 SQL<400
L26      12690 L25 AND SQL<400
```

=> file caplus		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	39.81	288.74
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	-6.57

FILE 'CAPLUS' ENTERED AT 17:15:34 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

```
=> s 126
L27      2552 L26

=> s 127 and PY<1987
      11536051 PY<1987
L28      1 L27 AND PY<1987
```

STN Columbus

=> d bib ab hitseq

L28 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987:13879 CAPLUS

DN 106:13879

TI Different human cervical carcinoma cell lines show similar transcription patterns of human papillomavirus type 18 early genes

AU Schneider-Gaedicke, Ansbert; Schwarz, Elisabeth

CS Inst. Virusforsch., Dtsch. Krebsforschungszent., Heidelberg, 6900, Fed. Rep. Ger.

SO EMBO Journal (1986), 5(9), 2285-92
CODEN: EMJODG; ISSN: 0261-4189

DT Journal

LA English

AB Transcription of human papillomavirus type 18 (HPV18) DNA in the human cervical carcinoma cell lines HeLa, C4-1 and SW756 was studied by nucleotide sequence anal. of HPV18-pos. cDNA clones isolated from a HeLa, C4-1 and SW756 cDNA library, resp., and the cDNA sequences were used to predict the potential encoded proteins. The cDNA clones from all 3 cell lines were found to be derived from virus-cell fusion transcripts in which 3'-terminal host cell sequences (different for each cell line) were spliced to 5'-terminal exon sequences from the HPV18 E6-E7-E1 region. Three different types of cDNA clones can be distinguished according to the splicing patterns obsd. in the 5' terminal HPV18 sequences. They carry as potential protein-coding regions the HPV18 specific open reading frames E6 and E6* (generated by splicing and identical with E6 up to the E6* splice junction), E7 and E1 (only in HeLa). Translation of specific cellular genes from the chimeric viral-cellular transcripts seem to be unlikely. The mapping of the 5'-ends of the virus-cell fusion transcripts indicates that transcription is initiated at a viral promoter. The similar patterns of HPV18 transcription in the 3 different cervical carcinoma cell lines suggest a functional role of HPV18 early genes for the malignant phenotype of these cells.

IT 105843-47-8

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 105843-47-8 CAPLUS

CN DNA (human papillomavirus 18 protein E 6* cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

```
SEQ      1 atggcgcgct ttgaggatcc aacacggcga cctacaagc tacctgatct
          51 gtgcacggaa ctgagcactt cactgcaaga catagaaata acctgtgtat
          101 attgcaagac agtattggaa cttacagagg tatttgaatt tgcattttaa
          151 gatttatttg tgggtgatag agacagtata ccgcgatgctg catgccataa
          201 atgtatagat ttttattcta gaattagaga attaagacat tattcagact
          251 ctgtgtatgg agacacattg gaaaaactaa ctaacactgg gttatacaat
          301 ttattaataa ggtgcctgcg gtgccagaaa ccgttgaatc cagcagaaaa
          351 acttag
```

=> file registry

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION

FULL ESTIMATED COST

10.74	299.48
-------	--------

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL
------------	-------

STN Columbus

	ENTRY	SESSION
CA SUBSCRIBER PRICE	-0.73	-7.30

FILE 'REGISTRY' ENTERED AT 17:17:25 ON 29 APR 2005
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 DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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 *
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 * effective March 20, 2005. A new display format, IDERL, is now *
 * available and contains the CA role and document type information. *
 *

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
 information enter HELP PROP at an arrow prompt in the file or refer
 to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s caaggggcc/sqen
      0 CAAGGGGCC/SQEN
      107453 SQL=9
L29      0 CAAGGGGCC/SQEN
          (CAAGGGGCC/SQEN AND SQL=9)
```

```
=> s caaggggcc/sqsn
L30      155151 CAAGGGGCC/SQSN
```

```
=> s 130 and SQL<400
      22713436 SQL<400
L31      13136 L30 AND SQL<400
```

=> file caplus		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	39.81	339.29
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	-7.30

FILE 'CAPLUS' ENTERED AT 17:18:38 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s l31
L32 2424 L31

=> s l32 and PY<1987
11536051 PY<1987
L33 1 L32 AND PY<1987

=> d bib ab hitseq

L33 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:124233 CAPLUS

DN 104:124233

TI Plasmid carrying sequences encoding salmon pituitary hormones or their precursors

IN Soma, Genichiro; Kitahara, Namiko; Okazaki, Hideo

PA Seikagaku Kogyo Co., Ltd., Japan

SO Jpn. Kokai Tokkyo Koho, 9 pp.

CODEN: JKXXAF

DT Patent

LA Japanese

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 60176588	A2	19850910	JP 1984-32700	19840224 <--
PPAI	JP 1984-32700		19840224		

AB Plasmids carrying base sequences encoding salmon pituitary hormones or their precursors are constructed. Base sequences that encode proopiomelanocorticotropin, corticotropin, α -melanotropin, corticotropin-like peptide, β -lipotropin, α -lipotropin, β -melanotropin, β -endorphin and salmon gonadotropin are given. Thus, mRNA isolated from the pituitary gland of salmon was used in the prepn. of cDNAs which were inserted into the PstI site of plasmid pBR322 for the transformation of Escherichia coli. Construction of plasmid pSSM17 (for transformation of E. coli for the prodn. of salmon precorticotropin) is given as an example.

IT 100984-20-1 100984-21-2

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 100984-20-1 CAPLUS

CN DNA, d(C-A-G-C-T-G-G-G-C-A-G-C-T-G-G-G-A-G-G-A-C-G-A-G-A-T-G-G-T-G-G-G-A-G-

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C-T-C-T-G-G-G-A-A-C-C-A-A-G-G-G-G-C-C-A-A-G-G-C-T-C-A-G-A-C-C-A-A-G-G-T-
A-G-T-C-C-C-A-G-A-A-C-C-T-C-A-C-T-G-T-G-A-C-G-G-G-G-C-T-G-C-A-A-G-A-T-
A-A-G-A-A-G-G-A-T-G-G-G-T-C-C-T-A-T-C-G-G-A-T-G-G-G-T-C-A-C-T-T-C-C-G-C-T-
G-G-G-G-C-A-G-C-C-C-A-A-C-C-G-C-T-A-T-C-A-A-G-C-G-C-T-A-C-G-G-T-G-G-C-T-T-
C-A-T-G-A-A-G-C-C-A-T-A-T-A-C-C-A-A-G-C-A-A-T-C-C-C-A-C-A-A-G-C-C-C-T-G-
A-T-C-A-C-G-C-T-G-C-T-C-A-A-G-C-A-C-A-T-C-A-C-C-C-T-T-A-A-G-A-A-C-G-A-G-C-
A-G) (9CI) (CA INDEX NAME)

NTE singlestranded

SEQ 1 cagctgggca gctgggagga cgagatgggtg ggagctctgg ggaaccaagg
51 ggccaaggct cagaccaagg tagtccccag aaccctcact gtgacggggc
101 tgcaagataa gaaggatggg tcctatcgga tgggtcactt ccgctggggc
151 agcccaaccg ctatcaagcg ctacgggtggc ttcatgaagc catataccaa
201 gcaatcccac aagcccctga tcacgctgct caagcacatc acccttaaga
251 acgagcag

RN 100984-21-2 CAPLUS

CN DNA, d(C-A-G-C-T-G-G-G-C-A-G-C-T-G-G-G-A-G-G-A-C-G-A-G-A-T-G-G-T-G-G-G-A-G-
C-T-C-T-G-G-G-G-A-A-C-C-A-A-G-G-G-G-C-C-A-A-G-G-C-T-C-A-G-A-C-C-A-A-G-G-T-
A-G-T-C-C-C-C-A-G-A-A-C-C-C-T-C-A-C-T-G-T-G-A-C-G-G-G-G-C-T-G-C-A-A-G-A-T-
A-A-G-A-A-G-G-A-T-G-G-G-T-C-C-T-A-T-C-G-G-A-T-G-G-G-T-C-A-C-T-T-C-C-G-C-T-
G-G-G-G-C-A-G-C-C-C-A-A-C-C-G-C-T-A-T-C) (9CI) (CA INDEX NAME)

NTE singlestranded

SEQ 1 cagctgggca gctgggagga cgagatgggtg ggagctctgg ggaaccaagg
51 ggccaaggct cagaccaagg tagtccccag aaccctcact gtgacggggc
101 tgcaagataa gaaggatggg tcctatcgga tgggtcactt ccgctggggc
151 agcccaaccg ctatc

=> file registry
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
10.74	350.03

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL
ENTRY	SESSION
-0.73	-8.03

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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```
*****
*
* The CA roles and document type information have been removed from *
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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*
*****
```

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s acggcaagg/sqen
      0 ACGGCAAGG/SQEN
107453 SQL=9
L34      0 ACGGCAAGG/SQEN
      (ACGGCAAGG/SQEN AND SQL=9)
```

```
=> s acggcaagg/sqsn
L35      140454 ACGGCAAGG/SQSN
```

```
=> s l35 and SQL<400
      22713436 SQL<400
L36      12155 L35 AND SQL<400
```

=> file caplus		
COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	39.81	389.84
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-8.03

FILE 'CAPLUS' ENTERED AT 17:21:41 ON 29 APR 2005
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 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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substance identification.

=> s 136

L37 2202 L36

=> s 137 and PY<1987\

NUMERIC VALUE NOT VALID '1987\'

Numeric values may contain 1-8 significant figures. If range notation is used, both the beginning and the end of the range must be specified, e.g., '250-300/MW'. Expressions such as '250-/MW' are not allowed. To search for values above or below a given number, use the >, =>, <, or <= operators, e.g., 'MW => 250'. Text terms cannot be used in numeric expressions. If you specify a unit, it must be dimensionally correct for that field code. To see the unit designations for field codes in the current file, enter "DISPLAY UNIT ALL" at an arrow prompt (=>).

=>

* * * * * RECONNECTED TO STN INTERNATIONAL * * * * *
SESSION RESUMED IN FILE 'CAPLUS' AT 17:22:26 ON 29 APR 2005
FILE 'CAPLUS' ENTERED AT 17:22:26 ON 29 APR 2005
COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)
COST IN U.S. DOLLARS

	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.45	390.29

	SINCE FILE	TOTAL
	ENTRY	SESSION
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	0.00	-8.03
CA SUBSCRIBER PRICE		

=> s 137 and PY<1987

11536051 PY<1987

L38 3 L37 AND PY<1987

=> d bib ab hitseq 1-3

L38 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:528776 CAPLUS

DN 105:128776

TI Cloning and sequencing of the gene encoding cytochrome c3 from
Desulfovibrio vulgaris (Hildenborough)

AU Voordouw, Gerrit; Brenner, Sydney

CS Dep. Biochem., Agric. Univ. Wageningen, Wageningen, NL-6703 BC, Neth.

SO European Journal of Biochemistry (1986), 159(2), 347-51

CODEN: EJBICAI; ISSN: 0014-2956

DT Journal

LA English

AB The gene encoding the redox protein cytochrome c3 [9035-44-3] from *D. vulgaris* (Hildenborough) was cloned using 2 synthetic oligonucleotides (one 17-mer and one 18-mer), designed to recognize the structural gene. Plasmid pCYC3 was derived from the clone and contains a 7.5 x 103-base EcoRI-HindIII insert of *D. vulgaris* DNA in pUC9. A 674-base-pair fragment of this insert was sequenced with the dideoxy-chain-termination procedure and found to contain the entire structural gene encoding cytochrome c3 bracketed by apparent *Escherichia coli* consensus for initiation and termination of transcription. The amino acid sequence of 107 residues, derived from protein sequencing, is confirmed by the nucleic acid sequence, which shows in addn. that it is preceded by a hydrophobic, pos. charged signal sequence of 21 residues. This N-terminal extension functions in the export of cytochrome c3, which is thought to reside in the periplasm of *D. vulgaris*.

STN Columbus

IT 104219-92-3

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 104219-92-3 CAPLUS

CN DNA (Desulfovibrio vulgaris clone pCYC3 cytochrome c3 gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaggaaac tgttttctg cgcggtactc gcccttgccg tagcctttgc
51 gctgccggtt gtggccgctc ccaaggcccc tggcgacggc ctgaagatgg
101 aagccaccaa gcagcccggtg gttttcaacc actccacca caagtccgtg
151 aagtgtggtg actgccacca ccccgatgaac ggcaaggaag actaccgcaa
201 gtgcggtacc gccgggtgcc acgacagcat ggacaagaag gacaagtccg
251 cgaagggtta ctacatgtc atgcatgaca agaacaccaa gttcaagtcc
301 tgcgtgggtt gccacgttga agtggccggt gccgatgccg ccaagaagaa
351 ggacctcacc ggctgaaga agtccaagt ccacgaatag

L38 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:573361 CAPLUS

DN 103:173361

TI Cloning and expression of the 1.3 S biotin-containing subunit of transcarboxylase

AU Murtif, Vicki L.; Bahler, Chris R.; Samols, David

CS Dep. Biochem., Case Western Reserve Univ., Cleveland, OH, 44106, USA

SO Proceedings of the National Academy of Sciences of the United States of America (1985), 82(17), 5617-21

====

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB The gene coding for the 1.3 S biotin-contg. subunit of transcarboxylase (EC 2.1.3.1) [9029-86-1] from *Propionibacterium shermanii* was cloned. Transcarboxylase is a well-characterized enzyme composed of 30 polypeptides of 3 different types; 12 1.3 S biotinyl subunits, 6 5 S dimeric outer subunits, and 1 12 S hexameric central subunit. In propionic acid fermn., the enzyme catalyzes the transfer of a carboxyl group from methylmalonyl-CoA to pyruvate in 2 partial reactions. The 1.3 S subunit binds the outer and central subunits of the enzyme together, and its biotin serves as carboxyl carrier between subsites on the central and outer subunits where each partial reaction occurs. The cloned gene was expressed in *Escherichia coli*, and the 1.3 S subunit accumulates to 7% of total cellular protein. The foreign protein is recognized and biotinylated by biotin holoenzyme synthetase of *E. coli*. The identifications of the gene and its product were confirmed by 4 independent approaches; DNA sequence anal., immunopptn., incorporation of labeled biotin, and measurement of enzymic activity in the 1st partial reaction.

IT 98824-75-0

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 98824-75-0 CAPLUS

CN DNA (*Propionibacterium shermanii* methylmalonyl coenzyme A carboxyltransferase biotinyl subunit gene) (9CI) (CA INDEX NAME)

SEQ 1 atgaaactga aggttaacagt caacggcact gcgtatgacg ttgacgttga
51 cgtcgacaag tcacacgaaa acccgatggg caccatcctg ttccggcgcg
101 gcaccggcgg cgcgccggca ccgcgcgag caggtggcgc aggcggcgg

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```

151 aaggccggag agggcgagat tcccgcctccg ctggccggca ccgtctccaa
201 gatcctcgtg aaggagggtg acacgggtcaa ggctgggtcag accgtgctcg
251 ttctcgaggc catgaagatg gagaccgaga tcaacgctcc caccgacggc
301 aaggtcgaga aggtccttgt caaggagcgt gacgccgtgc agggcggtca
351 ggtctcatc aagatcggt ga

```

L38 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1981:187080 CAPLUS

DN 94:187080

TI The nucleotide sequence of the hepatitis B viral genome and the identification of the major viral genes

AU Valenzuela, Pablo; Quiroga, Margarita; Zaldivar, Josefina; Gray, Patrick; Rutter, William J.

CS Dep. Biochem. Biophys., Univ. California, San Francisco, CA, 94143, USA

SO ICN-UCLA Symposia on Molecular Cellular Biology (1980), 18(Anim. Virus

====

Genet.), 57-70

CODEN: IUSMDJ; ISSN: 0097-9023

DT Journal

LA English

AB The complete sequence (3221 nucleotides) of the hepatitis B viral DNA (adw2 serotype) is reported. The long strand has 4 major polypeptide coding regions with an aggregate translational capacity of 1613 amino acids (4839 nucleotides). Two genes coding for the major viral proteins were identified: the previously described surface antigen gene coding for a protein of 25,398 daltons, and the core antigen gene, which codes for a basic polypeptide (21,335 daltons) with a striking protamine-like sequence at its C-terminus. There are 2 other putative peptide coding regions: A, which overlaps the surface antigen gene and may code for a protein up to ~95,000 daltons and B, which partially overlaps the core gene and may code for a peptide of ~16,000 daltons. The short strand of the virus is largely devoid of possible peptide coding regions. A single segment capable of coding a peptide of 94 amino acids is identified.

IT 77271-73-9

RL: PRP (Properties)

(nucleotide sequence of)

RN 77271-73-9 CAPLUS

CN DNA (hepatitis B virus subtype adw2 clone pEco-3/pBco-63/pPst-7 protein D gene) (9CI) (CA INDEX NAME)

NTE doublestranded

```

SEQ      1 agtagccttg actgttaaga cagcaggaga ggcctttat atgtagcaaa
        51 ggtaccgacg atccgacatg acggttgacc taggaagcgc cctgcaggaa
       101 acaaatgcag ggcagccgcg acttagggcg cctgctgggg agagccccgg
       151 cgaaccctga gagagcaggg gaagaggcag acggcaaggt cggctggtgc
       201 cccgcgtgga gagaaatgcg ccagaggggc agacacggaa gagtagacgg
       251 ccaggcacac gtgaagcgaa gtggagacgt gcaacgta

```

=> file registry

CCST IN U.S. DOLLARS

SINCE FILE

ENTRY

TOTAL

SESSION

FULL ESTIMATED COST

27.09

416.93

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DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-2.19	-10.22

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 DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s cgtacatcg/sqen
      0 CGTACATCG/SQEN
      107453 SQL=9
L39      0 CGTACATCG/SQEN
          (CGTACATCG/SQEN AND SQL=9)
```

```
=> s cgtacatcg/sqsn
L40      36728 CGTACATCG/SQSN
```

```
=> s l40 and SQL<400
      22713436 SQL<400
L41      4611 L40 AND SQL<400
```

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	39.81	456.74

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-10.22

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s 141
L42 769 L41

=> s 142 and PY<1987
11536051 PY<1987
L43 2 L42 AND PY<1987

=> d bib ab hitseq 1 2

L43 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:473434 CAPLUS

DN 105:73434

TI The trfB region of broad host range plasmid RK2: the nucleotide sequence reveals incC and key regulatory gene trfB/korA/korD as overlapping genes

AU Thomas, Christopher M.; Smith, Christopher A.

CS Dep. Genet., Univ. Birmingham, Birmingham, B15 2TT, UK

SO Nucleic Acids Research (1986), 14(11), 4453-69

CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB The nucleotide sequence of the trfB region of broad host range plasmid RK2 is reported. This region encodes the following loci: trfB, identical to korA and korD, which encodes a key transcriptional repressor of certain RK2 operons; incC, which appears to be involved in plasmid maintenance, possibly through post-transcriptional regulation of trfA product levels; the start of korB, which encodes a 2nd transcriptional repressor of operons involved in stable inheritance of RK2. These loci are expressed as part of the trfB operon. In combination with deletion anal., transcriptional and translation fusions and maxicell anal. of polypeptides, the DNA sequence allows a no. of conclusions to be drawn. First, the korB ORF start codon overlaps the incC ORF stop codon, suggesting the possibility of translational coupling between these 2 genes. Second, the trfB ORF lies entirely within the 1st third of the incC ORF using a different phase. Third, the incC ORF appears to contain a 2nd transcriptional start whose function appears to be coupled to translation of the trfB ORF. Anal. of codon usage in the region of overlap between incC and trfB suggests that the incC gene may have evolved before the trfB gene. Detn. of the DNA sequence of a mutant in which the product of trfB is rendered defective for transcriptional repression

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reveals an amino acid alteration within a region of this polypeptide which exhibits homol. to the α helix-turn- α helix motif characteristic of many DNA binding proteins, and which is probably responsible for recognition of the trfB operator by this protein.

IT 88748-47-4

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 88748-47-4 CAPLUS

CN DNA (plasmid RK2 gene korA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaagaaac ggcttaccga aagccagttc caggaggcga tccaggggct
51 ggaagtgggg cagcagacca tcgagatagc gcggggcgctc ttagtcgatg
101 ggaagccaca ggcgacgttc gcaacgtcgc tgggactgac caggggcgca
151 gtgtcgcaag cgggtcatcg cgtgtggggc gcgttcgagg acaagaactt
201 gcccagagggg tacgcgcggg taacggcggt tctgccggaa catcaggcgt
251 acatcgtcgg gaagtgggaa gcggacgcca agaaaaaaca ggaaaccaa
301 cgatga

L43 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:62573 CAPLUS

DN 100:62573

TI Map location and nucleotide sequence of korA, a key regulatory gene of promiscuous plasmid RK2

AU Bechhofer, David H.; Figurski, David H.

CS Dep. Microbiol., Coll. Phys. Surg., New York, NY, 10032, USA

SO Nucleic Acids Research (1983), 11(21), 7453-69

====

CODEN: NARHAD; ISSN: 0305-1048

LT Journal

LA English

AB Earlier work showed that the korA gene of the broad-host-range plasmid RK2 is located within the 50.4-56.4 region. By addnl. subcloning of this region, korA was mapped to the segment between the HaeII site at 55.0 and the HincII site at 55.6. The direction of korA transcription (55.6 to 55.1) was detd. by 2 methods: (1) inactivation of korA expression signals and fusion of the structural gene to other promoters; and (2) hybridization anal. of korA-specific RNA synthesized in vivo. The nucleotide sequence of the korA region was detd. A potentially strong promoter overlaps the HincII site at 55.6, and there is a coding region which specifies the putative korA polypeptide. That this is the korA gene was supported by sequence anal. of Bal31-generated deletion mutants of korA. The sequence shows the korA product to be a small basic polypeptide of 101 amino acids.

IT 88748-47-4

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 88748-47-4 CAPLUS

CN DNA (plasmid RK2 gene korA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaagaaac ggcttaccga aagccagttc caggaggcga tccaggggct
51 ggaagtgggg cagcagacca tcgagatagc gcggggcgctc ttagtcgatg
101 ggaagccaca ggcgacgttc gcaacgtcgc tgggactgac caggggcgca
151 gtgtcgcaag cgggtcatcg cgtgtggggc gcgttcgagg acaagaactt
201 gcccagagggg tacgcgcggg taacggcggt tctgccggaa catcaggcgt

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251 acatcgctcg gaagtgggaa gcgagcgcca agaaaaaaca ggaaaccaa
301 cgatga

=> file registry		
COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	19.59	476.33
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-1.46	-11.68

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<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s gtcagatcg/sqen
      0 GTCAGATCG/SQEN
107453 SQL=9
L44      0 GTCAGATCG/SQEN
      (GTCAGATCG/SQEN AND SQL=9)
```

```
=> s gtcagatcg/sqsn
L45      57217 GTCAGATCG/SQSN
```

```
=> s 145 and SQL<400
      22713436 SQL<400
L46      5041 L45 AND SQL<400
```


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=> file caplus
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
39.81	516.14

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL
ENTRY	SESSION
0.00	-11.68

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FILE 'CAPLUS' ENTERED AT 17:31:58 ON 29 APR 2005
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=> s l46
L47 1060 L46

=> s l47 and PY<1987
11536051 PY<1987
L48 0 L47 AND PY<1987

=> file registry
COST IN U.S. DOLLARS
FULL ESTIMATED COST

SINCE FILE	TOTAL
ENTRY	SESSION
2.34	518.48

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL
ENTRY	SESSION
0.00	-11.68

CA SUBSCRIBER PRICE

FILE 'REGISTRY' ENTERED AT 17:32:38 ON 29 APR 2005
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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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```
*****
*
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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*
*****
```

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s atgagggct/sqen
      C ATGAGGGCT/SQEN
      107453 SQL=9
L49      0 ATGAGGGCT/SQEN
          (ATGAGGGCT/SQEN AND SQL=9)
```

```
=> s atgagggct/sqsn
L50      161522 ATGAGGGCT/SQSN
```

```
=> s l50 and SQL<400
      22713436 SQL<400
L51      12306 L50 AND SQL<400
```

=> file caplus		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	39.81	558.29
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	-11.68

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STN Columbus

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=> s 151

L52 2438 L51

=> s 152 and PY<1987

11536051 PY<1987

L53 2 L52 AND PY<1987

=> d bib ab hitseq 1 2

L53 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:83873 CAPLUS

DN 104:83873

TI Synthesis and expression of the native RNase T1 gene and several mutant genes

AU Nishikawa, S.; Morioka, H.; Tokunaga, T.; Aoyama, Y.; Kikuyotani, S.; Fujimoto, K.; Yanase, K.; Tanaka, T.; Uesugi, S.; et al.

CS Fac. Pharm. Sci., Osaka Univ., Osaka, 565, Japan

SO Nucleic Acids Symposium Series (1985), 16(Symp. Nucleic Acids Chem., 13th), 287-90

CODEN: NACSD8; ISSN: 0261-3166

DT Journal

LA English

AB RNase T1 gene and several mutant genes were constructed by joining of chem. synthesized deoxyoligonucleotides. These genes were inserted into an expression vector and expressed as fused protein in Escherichia coli. RNase T1 and its mutant enzymes were liberated by CNBr treatment and their activities were measured.

IT 97708-04-8

RL: FRP (Properties)
(nucleotide sequence of)

RN 97708-04-8 CAPLUS

CN DNA, d(G-A-T-C-T-T-C-A-T-G-G-C-T-T-G-C-G-A-C-T-A-C-A-C-C-T-G-C-G-G-C-A-G-C-A-A-C-T-G-C-T-A-C-T-C-T-A-G-C-T-C-T-G-A-C-G-T-T-T-C-T-A-C-C-G-C-T-C-A-G-G-C-T-G-C-T-G-G-C-T-A-C-C-A-G-C-T-G-C-A-C-G-A-C-G-G-C-G-A-A-A-C-C-G-T-T-G-G-C-T-C-T-A-A-C-T-C-T-T-A-C-C-C-G-C-A-C-A-A-T-A-C-A-A-C-A-A-C-T-A-T-G-A-G-G-C-T-T-C-G-A-C-T-T-T-A-G-C-G-T-T-T-C-T-T-C-T-C-C-G-T-A-C-T-A-C-G-A-A-T-G-G-C-C-G-A-T-C-C-T-G-T-C-T-A-G-C-G-G-C-G-A-C-G-T-T-T-A-C-T-C-C-G-G-T-C-C-A-G-G-T-A-G-C-G-G-T-G-C-T-G-A-C-C-G-T-G-T-A-G-T-A-T-T-C-A-A-C-G-A-A-A-A-C-A-A-C-C-A-G-C-T-C-G-C-T-G-G-C-G-T-T-A-T-C-A-C-C-C-A-C-A-C-C-G-G-C-G-C-T-T-C-T-G-G-C-A-A-C-A-A-C-T-T-T-G-T-A-G-A-T-G-C-A-C-C-T-A-A-T-A-G), complex with DNA d(T-C-G-A-C-T-A-T-T-A-G-G-T-G-C-A-T-T-C-T-A-C-A-A-A-G-T-T-G-T-T-G-C-C-A-G-A-A-G-C-G-C-C-G-G-T-G-T-G-G-T-G-A-T-A-A-C-G-C-C-A-G-C-G-A-G-C-T-G-G-T-T-G-T-T-T-C-G-T-T-G-A-A-T-A-C-T-A-C-A-C-G-G-T-C-A-G-C-A-C-G-G-C-T-A-C-C-T-G-G-A-C-C-G-G-A-G-T-A-A-A-C-G-T-C-G-C-C-G-C-T-A-G-A-C-A-G-G-A-T-C-G-C-C-A-T-T-C-G-T-A-G-T-A-C-G-G-A-G-A-A-A-C-G-C-T-A-A-A-G-T-C-G-A-A-G-C-C-C-T-C-A-T-A-G-T-T-G-T-T-G-T-A-T-T-T-G-T-G-C-G-G-G-T-A-A-G-A-G-T-T-A-G-A-G-C-C-A-A-C-G-G-T-T-T-C-G-C-C-G-T-C-C-T-C-G-T-G-C-A-G-C-T-G-T-A-G-C-C-A-G-C-A-G-C-C-T-G-A-G-C-G-G-T-A-G-A-A-A-C-G-T-C-A-G-A-G-C-T-A-G-A-G-T-A-G-C-A-G-T-T-G-C-T-G-C-C-G-C-A-G-G-T-A-G-T-C-G-C-A-A-G-C-C-A-T-G-A-A) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 gatcttcatg gcttgcgact acacctgcgg cagcaactgc tactctagct
51 ctgacgtttc taccgctcag gctgctggct accagctgca cgaggacggc

STN Columbus

```

1  tgcactatta ggtgcattct acaaagttgt tgcagaagc gccggtgtgg
51  gtgataacgc cagcagctg  gttgttttcg ttgaatacta cacggtcagc
101 accgctacct ggaccggagt aaacgtcgcc gctagacagg atcggccatt
151 cgtagtacgg agaagaaacg ctaaagtcga agccctcata gttgttgtat
201 ttgtgcgggt aagagttaga gccaacggtt tcgccgtcct cgtgcagctg
251 tgagccagca gcctgagcgg tagaaacgtc agagctagct tagcagttgc
301 tqccqcaqqt qtaytcqcaa gccatgaa

```

Full Text

DN 103:82714

AU Ikehara, M.; Ohtsuka, E.; Uesugi, S.; Kikyodani, T.; Aoyama, Y.; Tokunaga, T.; Fujimoto, K.

50 Nucleic Acids Symposium Series (1984), 15(Symp. Nucleic Acids Chem.),

CODEN: NACSD8; ISSN: 0261-3166

LA : English

IT 97708-04-8P

```

      (prepn. cf, RNase T1 fusion protein expression from)

```

CN DNA, d(G-A-T-C-T-T-C-A-T-G-G-C-T-T-T-G-C-G-A-C-T-A-C-A-C-C-T-G-C-G-G-C-A-G-C-A-A-C-T-G-C-T-A-C-T-C-T-A-G-C-T-C-T-G-A-C-G-T-T-T-C-T-A-C-C-G-C-T-C-A-G-G-C-T-G-C-T-G-G-C-T-A-C-C-A-G-C-T-G-C-A-C-G-A-G-G-A-C-G-G-C-G-A-A-A-C-C-G-T-T-G-G-C-T-C-T-A-A-C-T-C-T-T-A-C-C-C-G-C-A-C-A-A-A-T-A-C-A-A-C-A-A-C-T-A-T-G-A-G-G-G-C-T-T-C-G-A-C-T-T-T-A-G-C-G-T-T-T-C-T-T-C-T-C-C-G-T-A-C-T-A-C-G-A-A-T-G-G-C-C-G-A-T-C-C-T-G-T-C-T-A-G-C-G-G-C-G-A-C-G-T-T-T-A-C-T-C-C-G-G-T-C-C-A-G-G-T-A-G-C-G-G-T-G-C-T-G-A-C-C-G-T-G-T-A-G-T-A-T-T-C-A-A-C-G-A-A-A-C-A-C-A-C-A-G-C-T-C-G-C-T-G-G-C-T-G-G-C-T-T-T-G-T-A-G-A-A-T-G-C-A-C-C-T-A-A-T-A-G), complex with DNA d(T-C-G-A-C-T-A-T-T-A-G-G-T-G-C-A-T-T-C-T-A-C-A-A-A-G-T-T-G-T-T-G-C-C-A-G-A-A-G-C-G-C-C-G-G-T-G-T-G-G-G-T-G-A-T-A-A-C-G-C-C-A-G-C-G-A-G-C-T-G-G-T-T-G-T-T-T-T-C-G-T-T-G-A-A-T-A-C-T-A-C-A-C-G-G-T-C-A-G-C-A-C-C-G-C-T-A-C-C-T-G-G-A-C-C-G-G-A-G-T-A-A-A-C-G-T-C-G-C-C-G-C-T-A-G-A-C-A-G-G-A-T-C-G-G-C-C-A-T-T-C-G-T-A-G-T-A-C-G-G-A-G-A-A-G-A-A-A-C-G-C-T-A-A-A-G-T-C-G-A-A-G-C-C-C-T-C-A-T-A-G-T-T-G-T-T-G-T-A-T-T-T-G-T-G-C-G-G-G-T-A-A-G-A-G-T-T-A-G-A-G-C-C-A-A-C-G-G-T-T-T-C-G-C-C-G-T-C-C-T-G-C-A-G-C-T-G-G-T-A-G-C-A-G-C-A-G-C-C-T-G-A-G-C-A-G-C-T-G-A-G-C-C-T-G-A-G-C-C-G-T-A-G-A-A-C-G-T-C-A-G-T-C-A-G-A-G-C-T-A-G-A-G-T-A-G-C-A-G-T-T-G-C-T-T-G-C-C-G-C-A-G-G-T-A-G-T-C-G-C-A-A-G-C-C-A-T-G-A-A) (1:1) (9CI) (CA INDEX NAME)

STN Columbus

NTE doublestranded (2)

```

SEQ      1 gatcttcatg gcttgcgact acacctgcgg cagcaactgc tactctagct
      51 ctgacgtttc taccgctcag gctgctggct accagctgca cgaggacggc
     101 gaaaccgttg gctctaactc ttaccgcgac aaatacaaca actatgaggg
     151 cttcgacttt agcgtttctt ctccgtacta cgaatggccg atcctgtcta
     201 gcggcgacgt ttactccggt ccaggtagcg gtgctgaccg tgtagtattc
     251 aacgaaaaca accagctcgc tggcgttatc acccacaccg gcgcttctgg
     301 caacaacttt gtagaatgca cctaatag

      1 tcgactatta ggtgcattct acaaagttgt tgccagaagc gccggtgtgg
      51 gtgataacgc cagcgagctg gttgttttcg ttgaatacta cacggtcagc
     101 accgctacct ggaccggagt aaacgtcgcc gctagacagg atcggccatt
     151 cgtagtacgg agaagaaacg ctaaagtcga agccctcata gttgttgat
     201 ttgtgcgggt aagagttaga gccaacggtt tcgccgtcct cgtgcagctg
     251 gtagccagca gcctgagcgg tagaaacgtc agagctagag tagcagttgc
     301 tgccgcaggt gtagtcgcaa gccatgaa
  
```

=> file registry		
COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
	18.69	576.98
FULL ESTIMATED COST		
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
	-1.46	-13.14
CA SUBSCRIBER PRICE		

FILE 'REGISTRY' ENTERED AT 17:35:59 ON 29 APR 2005
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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
 DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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TSOA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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 *
 * The CA roles and document type information have been removed from *
 * the IDE default display format and the ED field has been added, *
 * effective March 20, 2005. A new display format, IDERL, is now *
 * available and contains the CA role and document type information. *
 *

Crossover limits have been increased. See HELP CROSSOVER for details.
 Experimental and calculated property data are now available. For more

STN Columbus

information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s atgagcacg/sqsn
 L54 91801 ATGAGCACG/SQSN

=> s 154 and SQL<400
 22713436 SQL<400
 L55 6980 L54 AND SQL<400

=> file caplus	SINCE FILE	TOTAL
COST IN U.S. DOLLARS	ENTRY	SESSION
FULL ESTIMATED COST	32.53	609.51
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
CA SUBSCRIBER PRICE	ENTRY	SESSION
	0.00	-13.14

FILE 'CAPLUS' ENTERED AT 17:36:50 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s 155
 L56 1660 L55
 => s 155 and PY<1987
 1660 L55
 11536051 PY<1987
 L57 2 L55 AND PY<1987

=> d bib.ab hitseq 1 2

L57 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:210702 CAPLUS

DN 98:210702

TI Nucleotide sequence of bacteriophage λ DNA

AU Sanger, F.; Coulson, A. R.; Hong, G. F.; Hill, D. F.; Petersen, G. B.

CS Lab. Mol. Biol., Med. Res. Cent., Cambridge, CB2 2QH, UK

SO Journal of Molecular Biology (1982), 162(4), 729-73

STN Columbus

CODEN: JMOBAK; ISSN: 0022-2836

DT Journal

LA English

AB The nucleotide sequence of the DNA of phage λ was detd. by using the dideoxy chain termination method in conjunction with random cloning in phage M13 vectors. Various methods were studied for sequencing specific regions to complete the sequence, but all were much slower than the random approach. The DNA in its circular form contains 48,502 base pairs. Open reading frames were identified and, where possible, ascribed to genes by comparing with the previously detd. genetic map. The reading frames for 46 genes were clearly identified, though in -20, the position of the protein initiation site could not be rigorously established. Probable positions for the kil, cIII, and lom genes are suggested but remain uncertain. There are -20 other unidentified reading frames that may code for proteins. The genome is fairly compact with comparatively little noncoding DNA. In many cases, the translation terminators and initiators overlap, particularly in the sequence A-T-G-A where the TGA terminates 1 gene and the ATG initiates the next. Such structures seem to be characterized by a purine-rich sequence, rather than by a specific Shine and Dalgarno sequence, before the initiator. In the whole of the left arm, the codon CTA, which is normally read by a minor leucine tRNA, is absent. The distribution of other rare codons in the genes of the left arm suggests that they may have a controlling function of the relative amounts of the proteins produced.

IT 34616-07-9

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 34616-07-9 CAPLUS

CN DNA (coliphage λ gene ren) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgacgggca aagaggcaat tattcattac ctggggacgc ataatagctt
51 ctgtgcccgc gacgttgccg cgctaacagg cgcaacagta accagcataa
101 atcaggccgc ggctaaaatg gcacgggcag gtcttctggt tatcgaaggt
151 aaggtctggc gaacggtgta ttaccggttt gctaccaggg aagaacggga
201 aggaagatg agcacgaacc tgatttttaa ggagtgtcgc cagagtgccg
251 cgatgaaacg ggtattggcg gtatatggag ttaaagatg a

L57 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:66402 CAPLUS

DN 98:66402

TI A chain of interlinked genes in the ninR region of bacteriophage lambda

AU Kroeger, Manfred; Hobom, Gerd

CS Inst. Biol. III, Univ. Freiburg, Freiburg/Br., D-7900, Fed. Rep. Ger.

SO Gene (1982), 20(1), 25-38

====

CODEN: GENED6; ISSN: 0378-1119

DT Journal

LA English

AB The 3612-base-pair (bp) DNA sequence of the phage λ -P-Q (ninR) region contains a series of 9 open reading frames in a distinctly overlapping pattern: ATGA sequence modules occur at the boundaries of consecutive genes and are able to serve both as terminator (TGA) and (re)initiator (ATG) codons for most of the adjacent frames. Together with genes O, P, and Q, the newly detected ren and ninA through ninH constitute a series of 12 closely linked genes in the pR operon. The available evidence for several of the nin proteins, and plasmid expression data,

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suggest that at least the larger nin genes, and probably all of the newly detected open reading frames, code for proteins. The nin5 deletion of 2803 bp is a frame-to-frame fusion of ren and ninH, and covers the tr2 termination signal located near its left boundary, immediately behind the ren gene. The possible significance of the obsd. chain of closely interlinked genes for the regulation of Q expression is discussed.

IT 84616-07-9

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN: 84616-07-9 CAPLUS

CN: DNA (coliphage λ gene ren) (9CI) (CA INDEX NAME)

NFE doublestranded

```
SEQ      1 atgacgggca aagaggcaat tattcattac ctggggacgc ataatagctt
          51 ctgtgcccgc gacgttgccg cgctaacagg cgcaacagta accagcataa
          101 atcaggccgc ggctaaaatg gcacgggcag gtcttctggt tatcgaaggt
          151 aaggtctggc gaacggtgta ttaccggttt gctaccaggg aagaacggga
          201 aggaaagatg agcacgaacc tgatttttaa ggagtgtcgc cagagtgccg
          251 cgatgaaacg ggtattggcg gtatatggag taaaagatg a
```

=> file registry

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	18.69	628.20

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-1.46	-14.60

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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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```
*****
*
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* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*
*****
```

Crossover limits have been increased. See HELP CROSSOVER for details.

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Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s ggcgtgaac/sqsn
 L58 132811 GGC GTGAAC/SQSN

=> s 158 and SQL<400
 22713436 SQL<400
 L59 11658 L58 AND SQL<400

=> file caplus	SINCE FILE	TOTAL
COST IN U.S. DOLLARS	ENTRY	SESSION
	32.53	660.73
FULL ESTIMATED COST		
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
	0.00	-14.60
CA SUBSCRIBER PRICE		

FILE 'CAPLUS' ENTERED AT 17:39:48 ON 29 APR 2005
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FILE COVERS 1967 - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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=> s 159
 L60 1532 L59

=> s 160 and PY<1987
 11536051 PY<1987
 L61 0 L60 AND PY<1987

=> file registry	SINCE FILE	TOTAL
COST IN U.S. DOLLARS	ENTRY	SESSION
	2.34	663.07
FULL ESTIMATED COST		
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
	0.00	-14.60
CA SUBSCRIBER PRICE		

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FILE 'REGISTRY' ENTERED AT 17:40:33 ON 29 APR 2005
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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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*
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* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s atgatgatg/sqsn
L62 663450 ATGATGATG/SQSN

=> s 152 and SQL<400
22713436 SQL<400
L63 61649 L62 AND SQL<400

=> file caplus
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
32.53	695.60

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL
ENTRY	SESSION
0.00	-14.60

CA SUBSCRIBER PRICE

FILE 'CAPLUS' ENTERED AT 17:41:18 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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=> s 163

L64 5122 L63

=> s 164 and PY<1987

11536051 PY<1987

L65 11 L64 AND PY<1987

=> d bib ab hitseq 1-11

L65 ANSWER 1 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1989:19409 CAPLUS

DN 110:19409

TI Bacterial expression vectors containing lipoprotein gene 5' sequences

IN Mayne, Nancy G.; Burnett, J. Paul; Belegaje, Ramamoorthy; Hsiung, Hansen M.

PA Eli Lilly and Co., USA

SO U.S., 21 pp. Cont.-in-part of U.S. Ser. No. 381,992, abandoned.

CODEN: USXXAM

DT Patent

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 4745069	A	19880517	US 1984-586581	19840306
	HU 31783	O	19840528	HU 1983-1810	19830523 <--
	HU 197349	B	19890328		
PRAI	US 1982-381992	A2	19820525		

AB A plasmid for efficient expression of exogenous genes comprises the 5' untranslated region and promoter of the lipoprotein (lpp) gene operably linked to a translation start codon, a sequence encoding an enterokinase cleavage site, and the gene for the exogenous protein, as well as a replicon and ≥1 genes for selectable markers. Plasmid pCC101, contg. the Escherichia coli lpp gene 5' untranslated sequence and promoter and a gene encoding an enterokinase cleavage peptide fused to bovine growth hormone, was constructed. Fusion protein 240 mg was obtained from 22 g E. coli transformed with the plasmid. The biol. activity of the growth hormone released by enterokinase cleavage was comparable to that of a bovine growth hormone obtained from the National Pituitary Agency (as measured by proximal tibia epiphyseal cartilage growth in hypophysectomized female rats).

IT 119145-54-3

RL: PRP (Properties)

(enterokinase cleavage site-encoding double-stranded DNA, lipoprotein gene promoter-contg. microbial expression plasmids in relation to)

RN 118145-54-3 CAPLUS

CN Guanosine, 2'-deoxyguanylyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-

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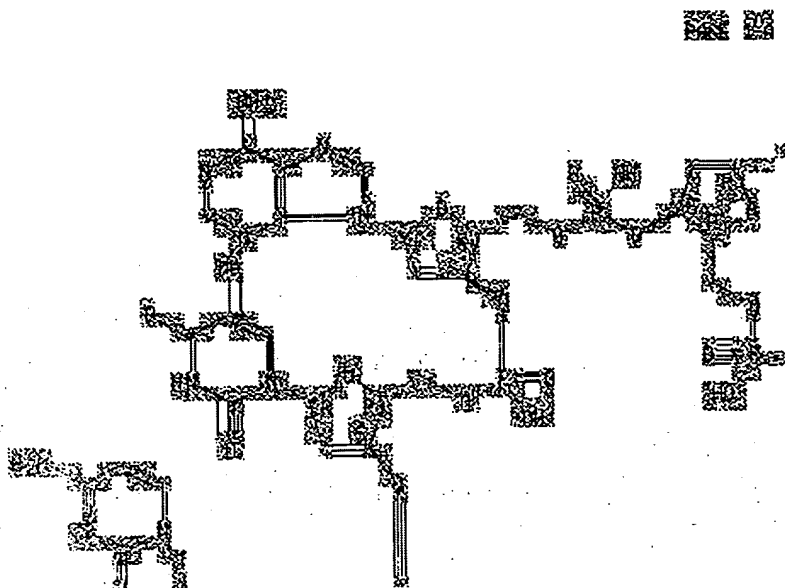
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 (3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-
 2'-deoxyadenylyl-(3'→5')-2'-adenylyl-(3'→5')-2'-deoxy-,
 complex with 2'-deoxycytidylyl-(3'→5')-thymidylyl-(3'→5')-
 thymidylyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-
 (3'→5')-2'-deoxycytidylyl-(3'→5')-2'-deoxyadenylyl-
 (3'→5')-thymidylyl-(3'→5')-2'-deoxycytidylyl-(3'→5')-
 2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxycytidine
 (1:1) (9CI) (CA INDEX NAME)

CM 1

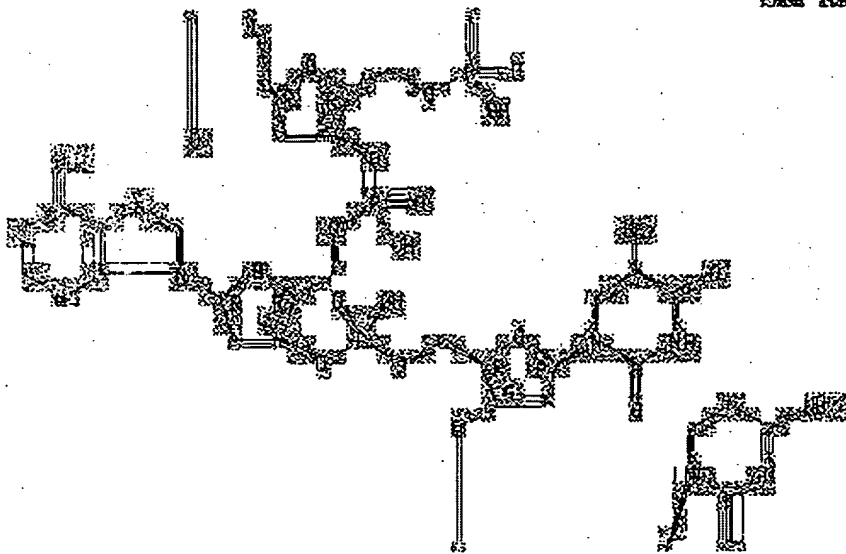
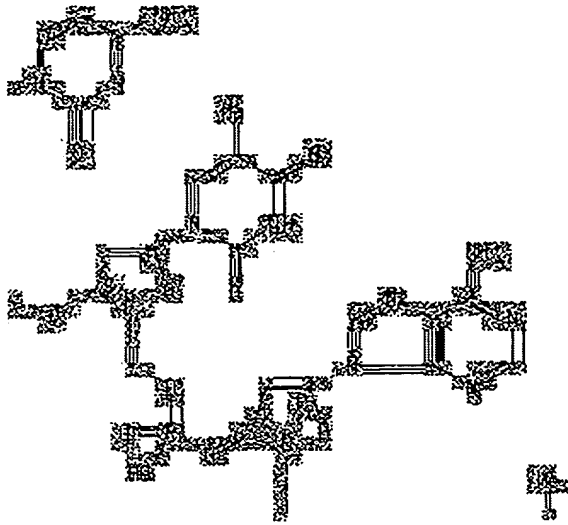
CRN 118145-53-2

CMF C116 H150 N37 O72 P11

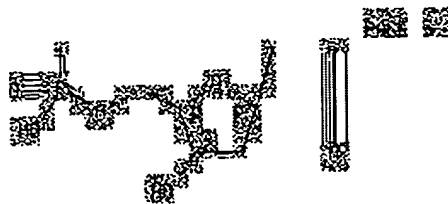
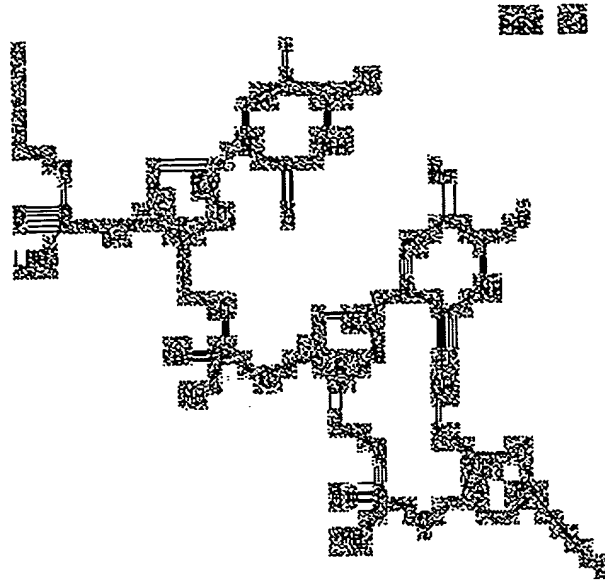
Absolute stereochemistry.



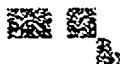
STN Columbus



STN Columbus



STN Columbus



CM 2

CRN 89233-95-4
CMF C150 H185 N63 O86 P14
CCI MAN

STRUCTURE DIAGRAM IS NOT AVAILABLE

IT 89382-91-2 89382-93-4

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of, lipoprotein gene promoter-contg. microbial
expression plasmids contg.)

RN 89392-91-2 CAPLUS

CN DNA, d(C-G-G-A-C-A-A-G-G-A-C-A-T-G-G-C-T-G-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-
A-T-C-C-A-A-T-G-G-G-A-A-C-A-T-T-A-T-T-A-A-T-A-C-C-C-T), complex with DNA
d(C-T-A-G-A-G-G-G-T-A-T-A-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-
T-G-A-T-A-A-G-T-T-C-C-C-A-G-C-C-A-T-G-T-C-C-T-T-G-T-C) (1:1) (9CI) (CA
INDEX NAME)

NTE doublestranded (2)

SEQ 1 ctatgagggtta ttaataatgt tccattgga tgatgatgat aagttccag
51 ccattgccctt gtc

1 cggacaagga catggctggg aacttatcat catcatccaa tgggaacatt
51 attaatacc t

RN 89382-93-4 CAPLUS

CN DNA, d(C-T-A-G-A-G-G-G-T-A-T-T-A-A-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-
G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-A-C-C-A-T-T-C-C-C-T-T-A-T-C-C-A-G-G-C-T-T-T-
T-T-G-A-C-A-A-C-G-C-T-A-T-G-C-T-C-C-G), complex with DNA
d(C-G-G-A-G-C-A-T-A-G-C-G-T-T-G-T-C-A-A-A-A-G-C-C-T-G-G-A-T-A-A-G-G-G-A-
A-T-G-G-T-T-G-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-A-T-C-C-A-A-T-G-G-G-A-A-C-A-
T-T-A-T-T-A-A-T-A-C-C-C-T) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 ctatgagggtta ttaataatgt tccattgga tgatgatgat aagttccaa
51 ccattgccctt atccaggctt ttgacaacg ctatgctccg

1 cggagcatag cgttgtcaaa aagcctggat aagggaatgg ttgggaactt
51 atcatcatca tccaatggga acattattaa taccct

STN Columbus

L65 ANSWER 2 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987:1101 CAPLUS

DN 106:1101

TI Origin of transfer of IncF plasmids and nucleotide sequences of the type II oriT, traM, and traY alleles from ColB4-K98 and the type IV traY allele from R100-1

AU Finlay, B. Brett; Frost, Laura S.; Paranchych, William

CS Dep. Biochem., Univ. Alberta, Edmonton, AB, T6G 2H7, Can.

SO Journal of Bacteriology (1986), 168(1), 132-9

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CODEN: JOBAAY; ISSN: 0021-9193

DT Journal

LA English

AB The complete nucleotide sequences of the ColB4-K98 (ColB4) plasmid transfer genes oriT, traM, and traY as well as the traY gene of plasmid R100-1 are presented and compared with the corresponding regions from the conjugative plasmids F, R1, and R100. The sequence encoding the oriT nick sites and surrounding inverted repeats identified in F was conserved in ColB4. The adenine-thymine-rich sequence following these nick sites was conserved in R1 and ColB4 but differed in F and R100, indicating that this region may serve as the recognition site for the traY protein. A series of direct repeats unique to the ColB4 plasmid was found in the region of dyad symmetry following this AT-rich region. This area also encodes 21-base-pair direct repeats which are homologous to those in F and R100. The traM gene product may bind in this region. Overlapping and following these repeats is the promoter(s) for the traM protein. The traM protein from ColB4 is similar to the equiv. products from F, R1, and R100. The traY protein from ColB4 is highly homologous to the R1 traY gene product, while the predicted R100-1 traY product differs at several positions. These differences presumably define the different alleles of traM and traY previously identified for IncF plasmids by genetic criteria. The translational start codons of the ColB4 and R100-1 traY genes are GUG and UUG, resp., 2 examples of rare initiator codon usage.

IT 105647-44-7

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 105647-44-7 CAPLUS

CN DNA (plasmid pED203 gene traM) (9CI) (CA INDEX NAME)

NTE doublestranded

```
SEQ      1 atggccagag taaatctgta tatcagtaat gaggttcattg aaaaaattaa
          51 catgattgtt gaaaagcgtc gtcaggaggg agcaagagat aaagatatata
          101 gccctttcagg aactgcttca atgcttcttg aattggggct tcgcgtatat
          151 gatgcacaga tggagcgtaa agagtctgctg tttaaccaga cagagtttaa
          201 taaacttctt cttgaatgtg ttgtaaaaac acagtcaacg gtggcuaaga
          251 ttttaggtat tgagtctctc agtctctcatg tctccggaaa ccgaagttt
          301 gaatatgccg gtatgggttg cgatatcaga gagaaagtgt ctgttgagat
          351 ggaccgggtt tttccaaaaa atgatgatga ataaatga
```

L65 ANSWER 3 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:181124 CAPLUS

DN 104:181124

TI Heat shock promoter and gene

IN Key, Joe L.; Gurley, William B.; Nagao, Ronald T.; Schoeffl, Friedrich; Czarnicka, Eva

PA Agrigenetics Research Associates Ltd., USA

STN Columbus

SO Eur. Pat. Appl., 52 pp.

CODEN: EPXXDW

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 159884	A2	19851030	EP 1985-302593	19850412 <--
	EP 159884	A3	19871125		
	EP 159884	B1	19930210		
	R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
	US 5447858	A	19950905	US 1984-599993	19840413
	CA 1338010	A1	19960130	CA 1985-478916	19850411
	JP 60248176	A2	19851207	JP 1985-79127	19850412 <--
	AT 85650	E	19930215	AT 1985-302593	19850412
	JP 07075567	A2	19950320	JP 1994-73623	19940412
PRAI	US 1984-599993	A	19840413		
	EP 1985-302593	A	19850412		

AB Four heat shock genes of soybean were cloned and sequenced. The heat shock promoter fragments of these 4 heat shock genes were subcloned and genetically engineered into a T-DNA shuttle vector. These recombinant vectors were then transferred with the aid of a helper plasmid into *Agrobacterium tumefaciens* where the recombinant DNA fragment was integrated into the Ti-plasmid. The T-DNA portion of the Ti-plasmid could then be transferred to a plant genome. Thus, the gene for β -galactosidase under the control of a soybean heat shock gene promoter was inserted into a T-DNA shuttle vector, p233G, and the recombinant plasmid was used to transform *Escherichia coli*. In a triple mating involving a helper plasmid in an *E. coli* strain, the recombinant T-DNA shuttle vector was transferred in another *E. coli* strain, and a Ti-plasmid in *A. tumefaciens*. The recombinant T-DNA shuttle vector was transferred into *A. tumefaciens* and the recombinant gene was incorporated into the Ti-plasmid. When plant cell cultures were infected with the *A. tumefaciens* carrying the recombinant Ti-plasmid the T-DNA was transferred to the plant genome. Transformed plant cells were detectable by the transient appearance of a blue color when the cells were subjected to heat shock in 5-bromo-4-chlor-3-indcyl- β -D-galactoside.

IT 102036-84-0 102036-85-1

RL: PRP (Properties)

(heat shock protein gene promoter encoding, of soybean)

RN 102036-84-0 CAPLUS

CN DNA, d(A-G-A-C-C-A-A-T-C-C-T-A-A-C-C-A-A-T-G-T-C-T-G-G-T-T-A-A-G-A-T-G-G-T-C-C-A-A-T-C-C-G-A-A-A-C-T-T-C-T-A-G-T-T-G-C-G-G-T-T-C-G-A-A-G-A-A-G-C-C-A-G-A-A-T-G-T-T-T-C-T-G-A-A-A-G-T-T-T-C-A-G-A-A-A-T-T-C-T-A-G-T-T-T-T-G-A-G-A-T-T-T-T-C-A-G-A-A-G-T-A-C-G-G-C-A-T-G-A-T-G-A-T-G-C-A-T-A-A-C-A-A-G-G-A-C-T-T-T-C-T-C-G-A-A-A-G-T-A-C-T-A-T-A-T-T-G-C-T-C-C-T-C-T-A-C-A-T-C-A-T-T-T-T-A-A-A-T-A-C-C-C-A-T-G-T-G-T-C-C-T-T-T-G-A-A-G-A-C-A-C-A-T-C-A-C-A-G-A-A-A-G-A-A-G-T-G-A-A-G-G-C-A-T-C-G-T-T-A-G-C-A-G-T-T-T-T-G-T-A-G-A-T-T-C-A-A-C-C-T-C-A-A-T-T-T-G-C-A-G-A-G-T-T-A-C-G-T-T-C-T-A-A-T-A-T-T-T-A-C-A-C-A-A-G-A-C-T-G-A-C-C-C) (9CI) (CA INDEX NAME)

NTE singlestranded

SEQ 1 agaccaatcc taaccaatgt ctggttaaga tggccaatc ccgaaacttc
51 tagttgcggt tcgaagaagc cagaatgttt ctgaaagttt cagaaaattc
101 tagttttgag attttcagaa gtacggcatg atgatgcata acaaggactt
151 tctcgaaagt actatattgc tcctctacat cattttaaat accccatgtg
201 tcctttgaag acacatcaca gaaagaagtg aaggcatcgt tagcagtttt
251 gtagattcaa cctcaatttg cagagttacg ttctaataata ttacacaag
301 actgaccc

STN Columbus

RN 102036-85-1 CAPLUS
 CN DNA, d(A-G-A-C-C-A-A-T-C-C-T-A-A-C-C-A-A-T-G-T-C-T-G-G-T-T-A-A-G-A-T-G-G-T-
 C-C-A-A-T-C-C-C-G-A-A-A-C-T-T-C-T-A-G-T-T-G-C-G-G-T-T-C-G-A-A-G-A-A-G-C-C-
 A-G-A-A-T-G-T-T-T-C-T-G-A-A-A-G-T-T-T-C-A-G-A-A-A-A-T-T-C-T-A-G-T-T-T-T-G-
 A-G-A-T-T-T-T-C-A-G-A-A-G-T-A-C-G-G-C-A-T-G-A-T-G-A-T-G-C-A-T-A-A-C-A-A-G-
 G-A-C-T-T-T-C-T-C-G-A-A-A-G-T-A-C-T-A-T-A-T-T-G-C-T-C-C-T-C-T-A-C-A-T-C-A-
 T-T-T-T-A-A-A-T-A-C-C-C-C-A-T-G-T-G-T-C-C-T-T-T-G-A-A-G-A-C-A-C-A-T-C-A-C-
 A-G-A-A-A-G-A-A-G-T-G-A-A-G-G-C-A-T-C-G-T-T-A-G-C-A-G-T-T-T-T-G-T-A-G-A-T-
 T-C-A-A-C-C-T-C-A-A-T-T-T-G-C-A-G-A-G-T-T-A-C-G-T-T-C-T-A-A-T-A-T-T-T-T-
 A-C-A-C-A-A-G-A-C-T-G-A-T-A-A-G-A-A-A-A-T-G-T-C-T-C-T-G-A-T-T-C-C-A-A-
 G-T-T-T-C-T-T-C-G-G-T-G-G-C-C-G-A-A-G-G-A-G-C-A-G-T-G-T-T-T-T-C-G-A-C-C-C-
 T-T-T-C-T-C-C-C-T-C-G-A-T-G-T-G-T-G-G) (9CI) (CA INDEX NAME)

NTE singlestranded

SEQ 1 agaccaatcc taaccaatgt ctgggtaaga tgggtccaatc ccgaaacttc
 51 tagttgcggt tcgaagaagc cagaatgttt ctgaaagttt cagaaaattc
 101 tagttttgag attttcagaa gtacggcatg atgatgcata acaaggactt
 151 tctcgaaagt acttatattgc tcctctacat cattttaaat accccatgtg
 201 tcctttgaag acacatcaca gaaagaagtg aaggcatcgt tagcagtttt
 251 gtagattcaa cctcaatttg cagagttacg ttctaataata ttacacaag
 301 actgataaga gaaaatgtct ctgattccaa gtttcttcgg tggccgaagg
 351 agcagtgttt tcgacccttt ctccctcgat gtgtgg

L65 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AM 1980:181123 CAPLUS
 DN 104:181123
 TI Vectors for expressing bovine growth hormone derivatives
 IN Hsiung, Hansen Maxwell; Schoner, Ronald George; Schoner, Brigitte
 Elisabeth
 PA Eli Lilly and Co., USA
 SO Eur. Pat. Appl., 105 pp.
 CODEN: EPXXDW
 DT Patent
 LA English
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 159123	A2	19851023	EP 1985-301468	19850304 <--
	EP 159123	A3	19870722		
	EP 159123	B1	19920115		
	R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
	ZA 8501625	A	19851029	ZA 1985-1625	19850304 <--
	AT 71659	E	19920215	AT 1985-301468	19850304
	SU 1838412	A3	19930830	SU 1985-3867006	19850304
	DK 8501000	A	19850907	DK 1985-1000	19850305 <--
	AU 8539503	A1	19850912	AU 1985-39503	19850305 <--
	AU 590716	B2	19891116		
	HU 38673	A2	19860630	HU 1985-835	19850305 <--
	HU 202281	B	19910228		
	ES 540935	A1	19870416	ES 1985-540935	19850305
	JP 61001391	A2	19860107	JP 1985-45685	19850306 <--
	CN 85101561	A	19860910	CN 1985-101561	19850401 <--
	ES 550873	A1	19871116	ES 1986-550873	19860114
	CA 1291718	A2	19911105	CA 1989-587903	19890110
PRAI	US 1984-586582	A	19840306		
	US 1984-634920	A	19840726		

STN Columbus

US 1985-697090 A 19850131
EP 1985-301468 A 19850304
CA 1985-475731 A3 19850305

AB Recombinant expression vectors are prepd. that comprise a runaway replicon and a transcriptional and translational activating sequence which is in the reading frame of a gene that codes for a bioactive bovine growth hormone (bGH) deriv. By cloning the bGH deriv. gene into vectors contg. a runaway replicon it is possible to induce loss of copy no. control. This results in a greatly increased rate of protein synthesis and the concomitant formation of a species of intracellular proteinaceous granule. These granules are highly homogeneous in their protein compn. and are thus distinguishable over known high-mol.-wt. aggregates and inclusions that sometimes occur in recombinant DNA-contg. host cells. Recombinant vectors contg. synthetic genes encoding thymosin $\alpha 1$, and human proinsulin and a runaway replicon were also prepd.

IT 89382-91-2P 89382-93-4P

RL: PREP (Preparation)

(prepn. of, as linker sequence for construction of bovine growth hormone plasmid vectors)

RN 89382-91-2 CAPLUS

CN DNA, d(C-G-G-A-C-A-A-G-G-A-C-A-T-G-G-C-T-G-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-A-T-C-C-A-A-T-G-G-G-A-A-C-A-T-T-A-T-T-A-A-T-A-C-C-C-T), complex with DNA d(C-T-A-G-A-G-G-G-T-A-T-T-A-A-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-G-C-C-A-T-G-T-C-C-T-T-G-T-C) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 ccagagggtta ttaataatgt tccattgga tgatgatgat aagttccag
51 ccattgccctt gtc
1 cgggacaagga catggtctggg aacttatcat catcatccaa tgggaacatt
51 ctaataacct t

RN 89382-93-4 CAPLUS

CN DNA, d(C-T-A-G-A-G-G-G-T-A-T-T-A-A-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-A-C-C-A-T-T-C-C-C-T-T-A-T-C-C-A-G-G-C-T-T-T-T-T-G-A-C-A-A-C-G-C-T-A-T-G-C-T-C-C-G), complex with DNA d(C-G-G-A-G-C-A-T-A-G-C-G-T-T-G-T-C-A-A-A-A-A-G-C-C-T-G-G-A-T-A-A-G-G-G-A-A-T-G-C-T-T-G-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-C-A-A-T-G-G-G-A-A-C-A-T-T-A-T-T-A-A-T-A-C-C-C-T) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 ccagagggtta ttaataatgt tccattgga tgatgatgat aagttccaa
51 ccattgccctt atccaggctt ttgacaacg ctatgctcg
1 cggagcatag cgttgtcaaa aagcctggat aagggatgg ttgggaactt
51 atcatcatca tccaatggga acattattaa taccct

L65 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:63384 CAPLUS

DN 104:63384

TI Recombinant DNA expression vectors and method for gene expression

IN Schoner, Ronald George; Schoner, Brigitte Elisabeth

PA Eli Lilly and Co., USA

STN Columbus

SO Eur. Pat. Appl., 118 pp.

CODEN: EPXXDW

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 154539	A2	19850911	EP 1985-301469	19850304 <--
	EP 154539	A3	19861230		
	R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
	ZA 8501626	A	19861029	ZA 1985-1626	19850304 <--
	SU 1491346	A3	19890630	SU 1985-3862498	19850304
	DK 9500999	A	19850907	DK 1985-999	19850305 <--
	AU 8539502	A1	19850912	AU 1985-39502	19850305 <--
	AU 589355	B2	19891012		
	HU 40162	A2	19861128	HU 1985-836	19850305 <--
	HU 202587	B	19910328		
	ES 540936	A1	19880501	ES 1985-540936	19850305
	CA 1283374	A1	19910423	CA 1985-475732	19850305
	JP 61001387	A2	19860107	JP 1985-45684	19850306 <--
	CN 85101555	A	19870124	CN 1985-101555	19850401
	ES 550013	A1	19870101	ES 1985-550013	19851216
	ES 550012	A1	19870601	ES 1985-550012	19851216

PRAI US 1984-586592 A 19840306

AB Recombinant DNA expression vectors which allow far more efficient gene expression are constructed. Thus, a XbaI-HgiAI DNA linker sequence was ligated to the ~10.2 kb BamHI-XbaI and ~0.6 kb BamHI-HgiAI fragments of plasmid pCZ101 to yield pCZ114. Plasmid pCZ114 contains, in sequence, the Escherichia coli lipoprotein gene transcriptional and translational activating sequences, a DNA sequence encoding the peptide Met-Phe-Pro-Leu-Glu-Asp-Asp, a stop codon, and a translational start signal which is immediately adjacent to and downstream from the stop signal and which is in the reading frame of a nucleotide sequence coding for methionyl-bovine growth hormone. Vectors are also constructed in which synthetic genes for thymosin $\alpha 1$ [62304-98-7] and human proinsulin [9035-68-1] were cloned, pTH $\alpha 1$ and pHI7 $\Delta 4\Delta 1$, resp.

IT 89382-91-2P 89382-93-4P

RL: PREP (Preparation)
(prepn. of)

RN 89382-91-2 CAPLUS

CN DNA, d(C-G-G-A-C-A-A-G-G-A-C-A-T-G-G-C-T-G-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-A-T-C-C-A-A-T-G-G-G-A-A-C-A-T-T-A-T-A-T-A-C-C-C-T), complex with DNA d(C-T-A-G-A-G-G-T-A-T-T-A-A-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-G-C-C-A-T-G-T-C-C-T-T-G-T-C) (1:1) (9CI) (CA INDEX NAME)

NTE Doublestranded (2)

SEQ 1 ctagagggta ttaataatgt tcccattgga tgatgatgat aagttccag
51 ccattgtcctt gtc

1 cggacaagga catggctggg aacttatcat catcatccaa tgggaacatt
51 attaataccc t

RN 89382-93-4 CAPLUS

CN DNA, d(C-T-A-G-A-G-G-G-T-A-T-T-A-A-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-A-C-A-T-T-T-C-C-C-T-T-A-T-C-C-A-G-G-C-T-T-T-T-T-G-A-C-A-A-C-G-C-T-A-T-G-C-T-C-C-G), complex with DNA d(C-G-G-A-G-C-A-T-A-G-C-G-T-T-G-T-C-A-A-A-A-G-C-C-T-G-G-A-T-A-A-G-G-G-A-

STN Columbus

A-T-G-G-T-T-G-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-C-A-A-T-G-G-G-A-A-C-A-T-T-A-T-T-A-A-T-A-C-C-C-T) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 ctagagggtta ttaataatgt tcccattgga tgatgatgat aagttcccaa
51 ccattccctt atccaggctt tttgacaacg ctatgctccg

1 cggagcatag cgttgtcaaa aagcctggat aaggggaatgg ttgggaactt
51 atcatcatca tccaatggga acattattaa taccct

L65 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:180056 CAPLUS

DN 102:180056

TI A single rearrangement event generates most of the chicken immunoglobulin light chain diversity

AU Reynaud, Claude Agnes; Anquez, Viviane; Dahan, Auriel; Weill, Jean Claude

CS Groupe Immunodifferentiation Mol., Inst. Jacques Monod, Paris, 75251, Fr.

SO Cell (Cambridge, MA; United States) (1985), 40(2), 283-91

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CODEN: CELLB5; ISSN: 0092-8674

DT Journal

LA English

AB The chicken Ig λ locus contains a single C λ gene with a unique J λ element, 1.9 kilobases (kb) upstream. The same V λ gene (V λ 1) is rearranged in most cells of the Bursa of Fabricius. This V λ 1 gene is located, in germ-line configuration, 1.7 kb upstream from J λ and in the same transcriptional orientation. Eight to 12 variable genes of the same set are found adjacent to the V λ 1 gene, indicating that V-gene amplification did occur. Three of these genes were sequenced and proved to be pseudogenes, one of them having an inverted polarity. Data suggesting extensive somatic diversification of the V λ 1 sequence are reported, including the possible use of nonfunctional V elements in a somatic gene-conversion-like process.

IT 96119-15-2

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 96119-15-2 CAPLUS

CN DNA (chicken immunoglobulin V λ 1 pseudogene ψ V1) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 gaggcctgt gccgcagtc acatgtggaa tatcaagaca cacacatcta
51 tgacaatcac aatctgatca tcaaccacta tggctggtac cagcagaggg
101 cacctggcag tgcacctgtc actctgatct actatgatga tgagagaccc
151 tcgaacatcc cttcacgatt ctccggttcc aaatccggct ccacacacac
201 attaacatc actggggtcc aagccgacga cgaggctgtc tattactgtg
251 ggaatgaaga cagcagcggc actggt

L65 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:605037 CAPLUS

DN 101:205037

STN Columbus

TI Nucleotide sequence encoding the flavoprotein and hydrophobic subunits of the succinate dehydrogenase of Escherichia coli
 AU Wood, David; Darlison, Mark G.; Wilde, Robin J.; Guest, John R.
 CS Dep. Microbiol., Sheffield Univ., Sheffield, S10 2TN, UK
 SO Biochemical Journal (1984), 222(2), 519-34

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CODEN: BIJOAK; ISSN: 0306-3275
 DT Journal
 LA English
 AB The nucleotide sequence of a 3614-base-pair (bp) segment of DNA contg. the sdhA gene, encoding the flavoprotein subunit of succinate dehydrogenase [9002-02-2] of E. coli, and the 2 genes sdhC and sdhD, encoding small hydrophobic subunits, was detd. Together with the Fe-S protein gene (sdhB), these genes form an operon (sdhCDAB) situated between the citrate synthase gene (gltA) and the 2-oxoglutarate dehydrogenase complex genes (sucAB): gltA-sdhCDAB-sucAB. Transcription of the gltA and sdhCDAB gene appears to diverge from a single intergenic region that contains 2 pairs of potential promoter sequences and 2 putative cAMP receptor protein-binding sites. The sdhA structural gene comprises 1761 bp (587 codons, excluding the initiation codon AUG), and it encodes a polypeptide of 64,263 mol. wt. that is strikingly homologous with the flavoprotein subunit of fumarate reductase (the frdA gene product). The FAD-binding region, including the histidine residue at the FAD-attachment site, was identified by its homol. with other flavoproteins and with the flavopeptide of the bovine heart mitochondrial succinate dehydrogenase. Potential active-site cysteine and histidine residues were also indicated by the comparisons. The sdhC (384 bp) and sdhD (342 bp) structural genes encode 2 strongly hydrophobic proteins of 14,167 and 12,792 mol. wt., resp. These proteins resemble in size and compn., but not sequence, the membrane anchor proteins of fumarate reductase (the frdC and frdD gene products).

IT 92941-88-3

RI: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)
 RN 92941-88-3 CAPLUS
 CN DNA (Escherichia coli gene sdhC) (9CI) (CA INDEX NAME)

NTE Doublestranded

SEQ 1 atgataagaa atgtgaaaaa acaaagacct gttaatctgg acctacagac
 51 catccgggttc cccatcacgg cgatagcgtc cattctccat cgcgtttccg
 101 gtgtgatcac ctttgttgca gtgggcatcc tgctgtggct tctgggtacc
 151 agcctctctt cccctgaagg ttctgagcaa gcttcgcga tbatgggcag
 201 cttcttcgct aaatttatca tgtggggcat ccttaccgct ctggcgtatc
 251 acgtcgctgt aggtattcgc cacatgatga tggattttgg ctatctggaa
 301 gaaacattcg aagcgggtaa acgctccgca aaaatctcct ttgttattac
 351 tgtcgtgctt tcacttctcg caggagccct cgtatggtaa

L65 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:133583 CAPLUS
 DN 100:133583
 TI Cloning vectors for expression of exogenous protein
 IN Mayne, Nancy Gail; Burnett, James Paul, Jr.; Belegaje, Ramamoorthy;
 Hsiung, Hansen Maxwell
 PA Eli Lilly and Co., USA
 SO Eur. Pat. Appl., 61 pp.
 CODEN: EPXXDW
 DT Patent

STN Columbus

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 95361	A1	19831130	EP 1983-302935	19830523 <--
	EP 95361	B1	19890726		
	R: BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
	IL 68753	A1	19890131	IL 1983-68753	19830522
	GB 2121054	A1	19831214	GB 1983-14183	19830523 <--
	GB 2121054	B2	19860226		
	DK 8302306	A	19831126	DK 1983-2306	19830524 <--
	AU 8314912	A1	19831201	AU 1983-14912	19830524 <--
	AU 560965	B2	19870430		
	JP 58219199	A2	19831220	JP 1983-92197	19830524 <--
	JP 07059193	B4	19950628		
	DD 210306	A5	19840606	DD 1983-251214	19830524 <--
	CA 1231068	A1	19880105	CA 1983-428700	19830524
	JP 66073096	A2	19940315	JP 1992-351893	19920917
PRAI	US 1982-381992	A	19820525		
	US 1982-382051	A	19820525		

AB A recombinant DNA cloning vector is constructed by ligating (a) a replication origin, (b) a selection marker gene (gene for ampicillin resistance), (c) and an in-tandem DNA sequence comprising a promoter for a lipoprotein control sequence, the 5' untranslated region of a lipoprotein expression-control sequence (lpp gene from a gram-neg. bacterium), and a start codon that is followed immediately by a sequence coding for an exogenous protein or by a sequence coding for an enterokinase [89382-91-2] cleavage site to which is immediately joined a sequence coding for an exogenous protein. When used as a cloning vector the lpp sequences control expression of exogenous DNA, but a nonhybrid protein product is formed; i.e. the translation product comprises methionine-optionally an enterokinase cleavage site-exogenous protein. Treatment with enterokinase removes the methionyl residue and leaves mature exogenous protein. Thus, to a plasmid contg. the Escherichia coli lipoprotein expression control sequence and plasmid pBR322 ampicillin-resistance genes was ligated a human growth hormone [12629-01-5] coding region with the use of a synthetic double-stranded DNA fragment complementary at 1 end to the natural lpp gene sequence (from the tbaI site through the initiating methionine codon), and at the other end, to the 1st 47 nucleotides of the gene for human growth hormone. The plasmid obtained, pNM645, was cloned in E. coli, and methionyl human growth hormone [82030-87-3] expression was verified by radioimmunoassay. The protein transcript represented 40% of the total protein with a yield of 22 million mols./cell. Biol. activity of the methionyl growth hormone with respect to proximal epiphyseal cartilage width in hypophysectomized female rats was the same as that of human growth hormone from cadavers.

IT 89382-91-2P

RL: PREP (Preparation)

(prepn. of, cattle growth hormone plasmid cloning vector construction in relation to)

RN 89382-91-2 CAPLUS

CN DNA, d(C-G-G-A-C-A-A-G-G-A-C-A-T-G-G-C-T-G-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-A-T-C-C-A-A-T-G-G-G-A-A-C-A-T-T-A-T-T-A-A-T-A-C-C-C-T), complex with DNA d(C-T-A-G-A-G-G-G-T-A-T-T-A-A-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-G-C-C-A-T-G-T-C-C-T-T-G-T-C) (1:1) (9CI) (CA INDEX NAME)

STRUCTURE DIAGRAM IS NOT AVAILABLE

IT 89382-93-4P

RL: PREP (Preparation)

STN Columbus

(prepn. of, human growth hormone plasmid cloning vector construction in relation to)

RN 89382-93-4 CAPLUS
CN DNA, d(C-T-A-G-A-G-G-T-A-T-T-A-A-T-A-A-T-G-T-T-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-A-C-C-A-T-T-C-C-C-T-T-A-T-C-C-A-G-G-C-T-T-T-T-T-G-A-C-A-A-C-G-C-T-A-T-G-C-T-C-C-G), complex with DNA
d(C-G-G-A-G-C-A-T-A-G-C-G-T-T-G-T-C-A-A-A-A-G-C-C-T-G-G-A-T-A-A-G-G-G-A-A-T-G-G-T-T-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-A-A-T-G-G-G-A-A-C-A-T-T-A-T-T-A-A-T-A-C-C-C-T) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 ctagagggtta ttaataatgt tccattgga tgatgatgat aagttcccaa
51 ccattccctt atccaggctt ttgacaacg ctatgctcgg

1 cggagcatag cggtgtcaaa aagcctggat aaggggaatgg ttgggaactt
51 atcatcatca tccaatggga acattattaa taccct

L65 ANSWER 9 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:120463 CAPLUS

DN 98:120463

TI Promoter mapping and DNA sequencing of the F plasmid transfer genes traM and traJ

AU Thompson, Russell; Taylor, Linda

CS Inst. Virol., Univ. Glasgow, Glasgow, G11 5JR, UK

SO Molecular and General Genetics (1982), 138(3), 513-18

====

CODEN MGGEAE; ISSN: 0026-8925

DT Journal

LA English

AB The nucleotide sequence of the DNA encoding the traM and finP genes as well as the promoter proximal segment of the traJ gene of the F plasmid was detd. The predicted amino acid sequence for the traM protein shows that this inner-membrane protein has no signal sequence. The promoters for both the traM and traJ genes were mapped by in vitro transcription and nuclease S1 protection expts. No unambiguous location can be assigned to the finP gene, but all candidates, if translated, would encode small proteins of between 24 and 52 amino acids.

IT 85030-89-3

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

PN 85030-89-3 CAPLUS

CN DNA (plasmid F gene traM) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggctaagg tgaacctgta tatcagcaat gatgcctatg aaaaaataaa
51 tgcgattatt gagaagcgtc gacaggaagg ggcaaggga aaagatgtca
101 gtttttcagc aacagcttca atgcttcttg aactggggct tcgtgtacat
151 gaggcctcaga tggagcgtaa agagtctgca tttaatcaga ctgagtttaa
201 taaattgctt cttgaatgct ttgtaaaaac acaatcatca gtagcgaaaa
251 ttttgggtat tgagtctctc agtcctcatg tctccggaaa ttcaaagttt
301 gaatatgcca atatggttga agatatcagg gagaaggat catctgagat
351 ggaacgattt ttccaaaaaa atgatgatga ataa

STN Columbus

L65 ANSWER 10 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1982:401504 CAPLUS

DN 97:1504

TI The two yeast histone H2A genes encode similar protein subtypes

AU Choe, Joonho; Kolodrubetz, David; Grunstein, Michael

CS Mol. Biol. Inst., Univ. California, Los Angeles, CA, 90024, USA

SO Proceedings of the National Academy of Sciences of the United States of America (1982), 79(5), 1484-7

====

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB The sequences of the 2 histone H2A genes in *Saccharomyces cerevisiae* were detd. These genes encode 2 histone H2A subtypes which are 131 amino acids in length but differ at 2 amino acid positions: an alanine → threonine and threonine → alanine change at positions 124 and 125. Thus, the 2 histone H2A subtypes have identical amino acid compns. The coding regions of the two H2A genes are homologous at 369 of 393 bases (94%), with all but 2 of the 24 changes being silent. There is only 30% homol. in the 5' flanking sequences of the two H2A genes. Like other eukaryotic histone genes, the yeast H2A genes are not interrupted by intervening sequences. When the yeast H2A histones are compared to those from other eukaryotes, there is ≥80% homol. in amino acid sequence.

IT 82029-65-0

RI: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 32029-65-0 CAPLUS

CN DNA (*Saccharomyces cerevisiae* histone H2A2 gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgtccggtg gtaaagggtg taaagctggt ccagctgcta aagcttctca
51 atctagatct gctaaagctg gtttaacatt cccagttggt agagtgcaca
101 gattgctaag aagaggtaac tacgccaga gaattgggtc tgggtgctca
151 gtctatctga ctgctgtctt agaatatctg gctgctgaaa ttttagaatt
201 ggctggtaat gctgctagag ataacaaaaa aaccagaatt attccaagac
251 atttacaatt ggccatcaga aatgatgatg aattgaacaa gctattgggt
301 aatgttacca tcgcccaagg tgggtgtttg ccaaaccatt accaaaactc
351 gttgccaag aagctctgcca agactgcca agcttctcaa gaactgtaa

L65 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1982:16954 CAPLUS

DN 96:16954

TI Deoxynucleotide linkers to be attached to a cloned DNA coding sequence

IN Rutter, William J.

PA University of California, Berkeley, USA

SO Eur. Pat. Appl., 41 pp.

CODEN: EPXXDW

DT Patent

LA English

FAN: CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 35394	A2	19810909	EP 1981-300826	19810227 <--
	EP 35384	A3	19820908		
	EP 35384	B1	19870610		

R: BE, CH, DE, FR, GB, IT, NL, SE

STN Columbus

CA 1200773	A1	19860218	CA 1981-371674	19810225 <--
ZA 8101308	A	19820331	ZA 1981-1308	19810226 <--
DK 8100888	A	19810830	DK 1981-888	19810227 <--
DK 166784	B1	19930712		
AU 8167922	A1	19810903	AU 1981-67922	19810227 <--
AU 545394	B2	19850711		
JP 56166200	A2	19811221	JP 1981-29294	19810228 <--
JP 06069375	B4	19940907		
IL 62237	A1	19850630	IL 1981-62237	19810301 <--
IL 71789	A1	19850630	IL 1981-71789	19810301 <--
IL 71790	A1	19850630	IL 1981-71790	19810301 <--
IL 71791	A1	19850630	IL 1981-71791	19810301 <--
US 4769326	A	19880906	US 1984-599464	19840412
CA 1200774	A2	19860218	CA 1984-452925	19840426 <--
CA 1200775	A2	19860218	CA 1984-452926	19840426 <--
CA 1201075	A2	19860225	CA 1984-452927	19840426 <--
PRAI US 1980-125878	A	19800229		
CA 1981-371674	A3	19810225		
IL 1981-62237	A	19810301		
US 1982-403405	A1	19820720		

AB Specific oligonucleotide segments are prepd. and linked to a cloned DNA coding segment in sequence which confer desired functional properties on the expression of the protein coded by the DNA coding sequence. Thus, the prepn. of a cloned human proinsulin gene and a specific cleavage linker is described, as well as the joining of the 2. The cloned DNA sequence coding for human proinsulin is isolated and prepd., and the DNA linker sequence-5'-GATGATGATGATAAA-3' is chem. synthesized by the phosphotriester method of K. Itakura (1977). The linker sequence is blunt-end ligated to com. available HindIII linker which, when cleaved by HindIII endonuclease, yields a specific cleavage linker for insertion at a HindIII site. The product linker nucleotide sequences for both strands are AGCTTGGATGATGATGATAAA (plus strand) and ACCTACTACTACTATTT (minus strand). The specific cleavage linker is blunt-end ligated with the cloned human proinsulin gene to produce a deoxynucleotide sequence of the plus strand contg. 5'-HindIII linker-specific cleavage linker-human proinsulin gene-3'.

IT 80208-71-5P

ML: SPN (Synthetic preparation); PREP (Preparation)
(prepn. of, as translatable linker for mol. cloning)

RN 80208-71-5 CAPLUS

CN DNA, d(A-G-C-T-T-G-G-A-T-G-A-T-G-A-T-G-A-T-A-A-A) (9CI) (CA INDEX NAME)

SEQ 1 agcttggatg atgatgataa a

=> file registry

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

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FULL ESTIMATED COST

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DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

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TOTAL

ENTRY

SESSION

CA SUBSCRIBER PRICE

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s.tgccccact/sqsn
L66 182547 TGCCCCACT/SQSN

=> s.l66 and SQL<400
22712436 SQL<400
L67 13495 L66 AND SQL<400

	SINCE FILE	TOTAL
COST IN U.S. DOLLARS	ENTRY	SESSION
FULL ESTIMATED COST	32.53	818.99

	SINCE FILE	TOTAL
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	-22.63

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s 167

L68 2432 L67

=> s 168 and PY<1987

11536051 PY<1987

L69 2 L68 AND PY<1987

=> d bib ab hitseq 1 2

L69 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987:79507 CAPLUS

DN 105:79507

TI Sequences of liver cDNAs encoding two different mouse insulin-like growth factor I precursors

AU Bell, Graeme I.; Stempien, Michelle M.; Fong, Noel M.; Rall, Leslie R.

CS Chiron Corp., Emeryville, CA, 94608, USA

SO Nucleic Acids Research (1986), 14(20), 7873-82

CODEN: NARHAD; ISSN: 0305-1048

DE Journal

LA English

AB Some cDNAs encoding mouse liver insulin-like growth factor I (IGF-I) [5750-96-6] have been isolated and sequenced. Alternative RNA splicing results in the synthesis of two types of mouse IGF-I precursor that differ in the size and sequence of the COOH-terminal peptide. The sequences of the signal peptides, IGF-I moieties, and the first 16 amino acids of the COOH-terminal peptides or E-domains of the two precursors are identical. The sequence difference results from the presence in preproIGF-IB mRNA of a 52-base insertion which introduces a 17-amino acid segment into the COOH-terminal peptide of preproIGF-IB and also causes a shift in the reading frame of the mRNA. As a consequence of this insertion, the COOH-terminal 19 and 25 amino acids of mouse preproIGF-IA and -IB, resp., are different. The sequences of mouse and human preproIGF-IA are highly conserved and possess 94% identity. In contrast, the sequences of mouse and human preproIGF-IB are quite different in the region of the COOH-terminal peptide. A comparison of the sequences of mouse and human preproIGF-IB mRNA indicates that they are generated by different mol. mechanisms.

IT 106716-60-3

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 106716-60-3 CAPLUS

CN DNA (mouse clone migf1-2 insulin-like growth factor I cDNA) (9CI) (CA INDEX NAME)

NTE Doublestranded

SEQ 1 atgtcgtctt cacacctt ctacctggcg ctctgcttgc tcacctcac
51 cagctccacc acagctggac cagagaccct ttgcggggct gagctggtgg
101 atgtcttca gttcgtgtgt ggaccgaggg gcttttactt caacaagccc
151 acaggctatg gctccagcat tcggagggca cctcagacag gcattgtgga
201 tgagtgttgc ttccggagct gtgatctgag gagactggag atgtactgtg
251 cccactgaa gcctacaaa gcagcccgt ctatccgtgc ccagcggcac
301 actgacatgc ccaagactca gaaggaagta cattgaaga acacaagtag

STN Columbus

351 aggaagtgcg ggaacaaga cctacagaat gtag

L69 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:605219 CAPLUS

DN 101:205219

TI Cloning and sequencing of a sheep metallothionein cDNA

AU Peterson, M. Gregory; Lazdins, Ieva; Danks, David M.; Mercer, Julian F. B.

CS Birth Defects Res. Inst., R. Child. Hosp., Parkville, Australia

SO European Journal of Biochemistry (1984), 143(3), 507-11

====

CODEN: EJBACI; ISSN: 0014-2956

DT Journal

LA English

AB A partially purified metallothionein mRNA fraction from Cu-injected sheep liver was used to synthesize double-stranded cDNA, which was dC-tailed, annealed to dG-tailed plasmid pBR322, and used to transform Escherichia coli MC1061. Of 1500 recombinant clones, only 1 gave a pos. signal when screened with a mouse metallothionein 1 probe. This clone (pSMT-1) contained an insert which included the entire coding region of a sheep metallothionein, the whole 3'-untranslated region, part of the poly(A)-tail, and 25 bases of the 5'-untranslated region. DNA sequence anal. showed that this sheep metallothionein was very similar to other mammalian metallothioneins, except for a threonine to proline change at amino acid 27. The clone also contained a different polyadenylation signal d(A-G-T-A-A-A) from that usually found d(A-A-T-A-A-A). A comparison of the DNA sequence of the sheep metallothionein with those of other species revealed an interesting region of homol. close to the poly(A) addn. signal in the 3'-untranslated region of the mRNA.

IT 92942-24-0

RL PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 92942-24-0 CAPLUS

CN DNA (sheep clone pSMT-1 metallothionein cDNA) (9CI) (CA INDEX NAME)

MTE doublestranded

SEQ 1 atggacccga actgctctg cccactggc ggctctgca gctgcgctgg
51 ctctgcacc tgcaaggcct gcagatgcc ctctgcaag aagagctgct
101 gctcttgctg cctgtgtggc tgtgccaagt gtgcccagg ctgtgtctgc
151 aaaggggcct cggacaagt cagctgctgc gcctga

=> d his; log y

(FILE 'HOME' ENTERED AT 16:55:34 ON 29 APR 2005)

FILE 'REGISTRY' ENTERED AT 16:56:02 ON 29 APR 2005

L1 0 S TGCTTACAT/SQEN

L2 201666 S TGCTTACAT/SQSN

L3 14623 S L2 AND SQL<400

FILE 'REGISTRY' ENTERED AT 16:57:30 ON 29 APR 2005

L4 14623 S L3

L5 0 S L4 AND PY<1987

STN Columbus

FILE 'CAPLUS' ENTERED AT 16:58:18 ON 29 APR 2005
L6 2668 S L3
L7 4 S L6 AND PY<1987

FILE 'STNGUIDE' ENTERED AT 17:00:49 ON 29 APR 2005

FILE 'REGISTRY' ENTERED AT 17:03:34 ON 29 APR 2005
L8 0 S CACTCATAT/SQEN
L9 157456 S CACTCATAT/SQSN
L10 9780 S L9 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:04:45 ON 29 APR 2005
L11 2154 S L10
L12 1 S L11 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:07:46 ON 29 APR 2005
L13 0 S GAAGGTCCT/SQEN
L14 193989 S GAAGGTCCT/SQSN
L15 16920 S L14 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:08:58 ON 29 APR 2005
L16 2703 S L15
L17 4 S L16 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:12:32 ON 29 APR 2005
L18 0 S GGGAGTACG/SQEN
L19 116522 S GGGAGTACG/SQSN
L20 5701 S L19 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:13:47 ON 29 APR 2005
L21 1154 S L20
L22 0 S L21 AND PY<1987
L23 0 S L21 AND PY<1988

FILE 'REGISTRY' ENTERED AT 17:14:20 ON 29 APR 2005
L24 0 S GGTATTTGA/SQEN
L25 122237 S GGTATTTGA/SQSN
L26 12380 S L25 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:15:34 ON 29 APR 2005
L27 2552 S L26
L28 1 S L27 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:17:25 ON 29 APR 2005
L29 0 S CAAGGGGCC/SQEN
L30 155151 S CAAGGGGCC/SQSN
L31 13136 S L30 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:18:33 ON 29 APR 2005
L32 2424 S L31
L33 1 S L32 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:20:30 ON 29 APR 2005
L34 0 S ACGGCAAGG/SQEN
L35 140454 S ACGGCAAGG/SQSN
L36 12155 S L35 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:21:41 ON 29 APR 2005
L37 2202 S L36
L38 3 S L37 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:25:55 ON 29 APR 2005

STN Columbus

L39 0 S CGTACATCG/SQEN
L40 36728 S CGTACATCG/SQSN
L41 4611 S L40 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:27:16 ON 29 APR 2005

L42 769 S L41
L43 2 S L42 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:30:53 ON 29 APR 2005

L44 0 S GTCAGATCG/SQEN
L45 57217 S GTCAGATCG/SQSN
L46 5041 S L45 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:31:58 ON 29 APR 2005

L47 1060 S L46
L48 0 S L47 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:32:38 ON 29 APR 2005

L49 0 S ATGAGGGCT/SQEN
L50 161522 S ATGAGGGCT/SQSN
L51 12306 S L50 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:33:33 ON 29 APR 2005

L52 2438 S L51
L53 2 S L52 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:35:59 ON 29 APR 2005

L54 91301 S ATGAGCACG/SQSN
L55 8980 S L54 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:36:50 ON 29 APR 2005

L56 1360 S L55
L57 2 S L55 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:38:57 ON 29 APR 2005

L58 112811 S GCGTGAAC/SQSN
L59 11658 S L58 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:39:48 ON 29 APR 2005

L60 1832 S L59
L61 0 S L60 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:40:33 ON 29 APR 2005

L62 663450 S ATGATGATG/SQSN
L63 62649 S L62 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:41:18 ON 29 APR 2005

L64 5122 S L63
L65 11 S L64 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:47:08 ON 29 APR 2005

L66 182547 S TGCCCCACT/SQSN
L67 13495 S L66 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:47:56 ON 29 APR 2005

L68 2432 S L67
L69 2 S L68 AND PY<1987

COST IN U.S. DOLLARS
FULL ESTIMATED COST

SINCE FILE
ENTRY
18.24

TOTAL
SESSION
837.23

STN Columbus

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-1.46	-24.09

STN INTERNATIONAL LOGOFF AT 17:49:39 ON 29 APR 2005

AN 1982:46833 CAPLUS
DN 96:46833
TI Regulation of the S10 ribosomal protein operon in E. coli: nucleotide
sequence at the start of the operon
AU Olins, Peter O.; Nomura, Masayasu
CS Inst. Enzyme Res., Univ. Wisconsin, Madison, WI, 53706, USA
SO Cell (Cambridge, MA, United States) (1981), 26(2, Pt. 2), 205-11

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CODEN: CELLB5; ISSN: 0092-8674

DT Journal

LA English

AB The DNA sequence of a 1250-base-pair segment of the Escherichia coli chromosome that carries the promoter for the S10 ribosomal protein operon, the S10 gene, and part of the L3 gene was detd. A DNA fragment carrying the putative S10 promoter was cloned into the plasmid mini-Col E1, which contains a transcription termination signal close to the single HindII site. Cells harboring the hybrid plasma produced a relatively stable hybrid mRNA with the expected sequence, demonstrating that the promoter functions in vivo. Comparison of the mRNA sequence around the start of the S10-coding region, the presumed target site for L4 repressor protein, with the known binding site for L4 on 23 S rRNA revealed the presence of sequence homologies. This supports the model of the translational feedback regulation of the S10 operon by L4.

IT 80451-23-6

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 80451-23-6 CAPLUS

CN DNA (Escherichia coli ribosome protein S 10 gene) (9CI) (CA INDEX NAME)

SEQ 1 atgcagaacc aaagaatccg tatccgcctg aaagcgtttg atcatcgtct
51 gatcgatcaa gcaaccgcgg aaatcgtcga gactgccaag cgcactggtg
101 cgcaggtccg tgggtccgatc ccgctgccga cacgcaaaga gcgcttcact
151 gttctgatct ccccgcacgt caacaaagac gcgcgcgatc agtacgaaat
201 ccgtactcac ttgcgtctgg ttgacatcgt tgagccaacc gagaaaaccg
251 ttgatgctct gatgcgtctg gatctggctg ccggtgtaga cgtgcagatc
301 agcctggggtt aa

FLG1